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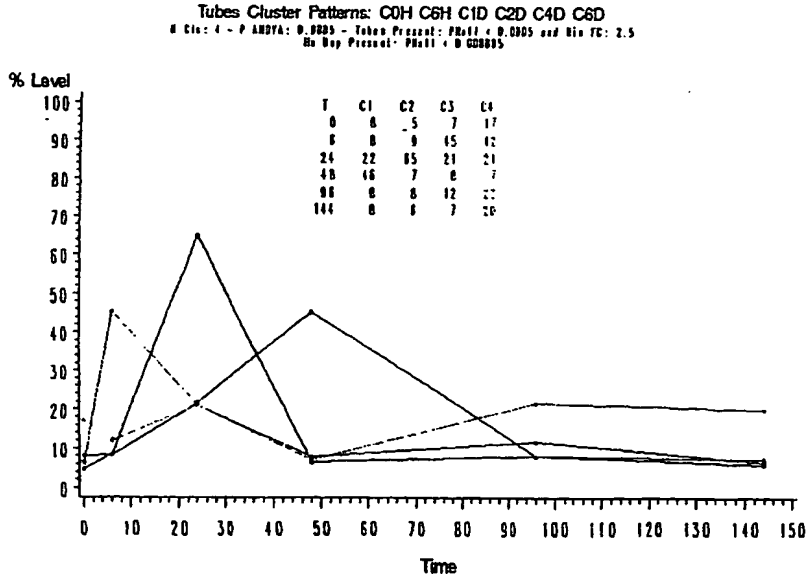


(57) Abstract: Described herein are methods that can be used for diagnosis of angiogenesis and angiogenic phenotypes. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate angiogenesis. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in disorders associated with angiogenesis are described.

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# NOVEL METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS AND METHODS OF SCREENING FOR ANGIOGENESIS MODULATORS

## FIELD OF THE INVENTION

The invention relates to the identification of expression profiles and the nucleic acids involved in angiogenesis, and to the use of such expression profiles and nucleic acids in diagnosis of angiogenesis. The invention further relates to methods for identifying candidate agents and/or targets which modulate angiogenesis.

## BACKGROUND OF THE INVENTION

New blood vessel development comprises the formation of veins (vasculogenesis) and arteries (angiogenesis). Angiogenesis plays a normal role in embryonic development, as well as menstration, wound healing. Angiogenesis also plays a crucial pathogenic role in a variety of disease states, including cancer, proliferative diabetic retinopathy, and maintaining blood flow to chronic inflammatory sites.

Angiogenesis has a number of stages. The early stages of angiogenesis include endothelial cell protease production, migration of cells and proliferation. The early stages also appear to require some growth factors, with VEGF, TGF-α, angiostatin, and selected chemokines all putatively playing a role. Later stages of angiogenesis include the population of the vessels with mural cells (pericytes or smooth muscle cells), basement membrane production and the induction of vessel bed specializations. The final stages of vessel formation include what is known as "remodeling", wherein a forming vasculature becomes a stable, mature vessel bed.

Thus, understanding the genes, proteins and regulatory mechanisms that occur during angiogenesis would be desirable. Accordingly, it is an object of the invention to provide methods that can be used to screen candidate bioactive agents for the ability to modulate angiogenesis. Additionally, it is an object to provide molecular targets for therapeutic intervention in disease states which either have an undesirable excess or a deficit in angiogenesis.

## SUMMARY OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for angiogenesis, as well as methods for screening for compositions which modulate angiogenesis. Methods of treatment of disorders associated with angiogenesis, as well as compositions are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in angiogenesis cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to an angiogenesis modulator protein (AMP), the method comprising combining the AMP and a candidate bioactive agent, and determining the binding of the candidate agent to the AMP. Preferably the AMP is a protein or fragment thereof selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of an AMP. In one embodiment the method comprises combining the AMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the AMP. Preferably the AMP is a protein or fragment thereof selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Also provided is a method of evaluating the effect of a candidate angiogenesis drug comprising administering the drug to a transgenic animal expressing or over-expressing the AMP, or an animal lacking the AMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate angiogenesis drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, the expression profile includes a gene of Table 1, Table 2, Table 3, Table 4 or Table 5.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments which encode an angiogenesis protein, preferable selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase , or fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Furthermore, a method of diagnosing a disorder associated with angiogenesis is provided. The method comprises determining the expression of a gene which encodes an angiogenesis protein preferable selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. A difference in the expression indicates that the first individual has a disorder associated with angiogenesis.

In another aspect, the present invention provides an antibody which specifically binds to an angiogenesis preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10 or fragment thereof. . In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. In a preferred embodiment the fragment of AAA1 is selected from AAA1p1 or AAA1p2. Other preferred fragments for the angiogenesis proteins are shown in the figures.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a angiogenesis modulating protein (AMP) or a fragment thereof and an antibody which binds to said AMP or fragment thereof. In a preferred embodiment, the method comprises combining an AMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said AMP or fragment thereof. The method further includes determining the binding of said AMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits angiogenesis.

In a further aspect, a method for inhibiting angiogenesis is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting angiogenesis is provided to an individual with a disorder associated with angiogenesis such as cancer. As described herein, methods of inhibiting angiogenesis can be performed by administering an inhibitor of the activity of an angiogenesis protein, including an antisense molecule to the gene or its gene products, and preferable small molecules.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin,

endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof, and a pharmaceutically acceptable carrier.

In another embodiment the nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

A method of neutralizing the effect of an angiogenesis protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

In another aspect of the invention, a method of treating an individual for a disorder associated with angiogenesis is provided. In one embodiment, the method comprises administering to said individual an inhibitor of Edg-1. In another embodiment, the method comprises administering to a patient having a disorder with angiogenesis an antibody to Edg-1 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

Novel sequences are provided herein. Compounds and compositions are also provided. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

## DETAILED DESCRIPTION OF THE TABLES AND FIGURES

Table 1 provides the Accession numbers for 1774 genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Table 2 provides the Accession numbers for a preferred subset of 559 genes, including expression sequence tags (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not. The sequences are characterized as predicted to encode secreted proteins (SS), or transmembrane proteins (TM) proteins.

Table 3 provides the Accession numbers for 1916 genes including expression sequence tags (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Table 4 provides a preferred subset of 558 Accession numbers identified in Figure 4 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Table 5 provides a preferred subset of 20 Accession numbers identified in Figure 4 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Figure 1 is a graph of expression levels of sequences identified in Figure 1. Expression profiles are clustered into 4 groups. C1 (blue), C2 (red), C3 (green) and C4 (mustard).

Figure 2 shows an embodiment of a nucleic acid (mRNA) which includes a sequence encoding an angiogenesis protein, AAA4. The start and stop codons are underlined.

Figure 3 shows the open reading frame of a nucleic acid sequence encoding AAA4. The start and stop codons are underlined.

Figure 4 shows an embodiment of the amino acid sequence of AAA4. The signal peptide is double underlined, and the transmembrane sequence is underlined. In one embodiment herein, AAA4 is soluble. Thus, the signal peptide can be omitted, and the transmembrane domain deleted, inactivated, or truncated.

Figure 5 shows peptides AAA4p1 and AAA4p2.

Figure 6 shows the expression of AAA4 in angiogenesis models over time and in other, non-angiogenic tissues.

Figure 7 shows an embodiment of a nucleic acid sequence encoding an angiogenesis protein, AAA1. A putative stop codon is underlined.

Figure 8 shows an embodiment of an amino acid sequence for AAA1. A transmembrane domain is underlined. In one embodiment, AAA1 is soluble. In preferred embodiments, the transmembrane domain is deleted or inactivated, or AAA1 is truncated to delete the transmembrane domain.

Figure 9 shows AAA1p1 and AAA1p2.

Figure 10 shows a graph showing the relative expression of AAA1 in various tissues at different time points. "Exp 3" is an angiogenesis model showing tube formation over time using endothelial cells.

Figure 11 shows an embodiment of a nucleic acid, mRNA, which comprises a sequence encoding an angiogenesis protein, Edg-1. The start and stop codons are underlined.

Figure 12 shows the open reading frame encoding Edg-1, wherein the start and stop codons are underlined.

Figure 13 shows an embodiment of an amino acid sequence for an angiogenesis protein, Edg-1, wherein the transmembrane domains are underlined. In a preferred embodiment herein, a soluble form of Edg-1 is provided. In one embodiment, the transmembrane domains are deleted, inactivated, and/or the protein is truncated so as to exclude the domains (with or without re-ligation of remaining soluble regions).

Figure 14 depicts four peptide sequences provided herein and their respective solubilities.

Figure 15 shows the expression of Edg-1 over a variety of tissues.

Figure 16 shows the time course of induction of Edg-1 in a model for angiogenesis (Expt 1, Expt 2, Expt 3) in which low passage human endothelial cells form into tube structures over a period of a few

days in culture. The reproducible induction of Edg-1 occurred in a time frame consistent with its role in the tube forming process.

Figure 17 shows an embodiment of a nucleic acid sequence which includes the coding sequence for a tissue remodeling protein, alpha 5 beta 1 integrin (sometimes referred to as VLA-5), wherein the start and stop codon are underlined.

Figure 18 shows an embodiment of an amino acid sequence of a tissue remodeling protein, alpha 5 beta 1 integrin, wherein a transmembrane domain is underlined.

Figure 19 shows a bar graph depicting the results of 5 expression profiles of alpha 5 beta 1 integrin throughout the time course of tube formation. In particular, tube models 1, 2 and 3 show models which form tube structures from single isolated human endothelial cells; the "EC/PMA" model shows endothelial cells stimulated with pokeweed mitogen antigen, and the body atlas profile shows expression in various normal cell types and tissues.

Figures 20A and 20B show the results of antagonism of tube formation wherein Figure 20A is an isotype control and Figure 20B shows specific antibody antagonism after 48 hours.

Figure 21 shows an embodiment of a nucleic acid sequence which includes the coding sequence for an angiogenesis protein, endomucin, wherein the start and stop codon are boxed.

Figure 22 shows an embodiment of an amino acid sequence of an angiogenesis protein, endomucin, wherein a signal sequence is bolded and a transmembrane domain is underlined.

Figure 23 shows an embodiment of a nucleic acid sequence which includes the coding sequence for an angiogenesis protein, matrix metalloproteinase 10 (also called stromolysin 2), wherein the start and stop codon are boxed.

Figure 24 shows expression of matrix metalloproteinase 10 over a variety of tissues.

Figure 25 shows expression of matrix metalloproteinase 10 over a variety of tissues.

## DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis of disorders associated with angiogenesis (sometimes referred to herein as angiogenesis disorders or AD), as well as methods for screening for compositions which modulate angiogenesis. By "disorder associated with angiogenesis" or "disease associated with angiogenesis" herein is meant a disease state which is marked by either an excess or a deficit of vessel development. Angiogenesis disorders include, but are not limited to, cancer and proliferative diabetic retinopathy. Also provided are method for treating AD.

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from AD tissue. By comparing expression profiles of tissue in known different angiogenesis states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in angiogenic versus non-angiogenic tissue allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate angiogenesis and thus tumor growth or recurrence in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the angiogenic expression profile. This may be done by making biochips comprising sets of the important angiogenesis genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the angiogenic proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the angiogenic nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the angiogenic proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in angiogenesis, herein termed "angiogenesis sequences". As outlined below, angiogenesis sequences include those that are up-regulated (i.e. expressed at a higher level) in disorders associated with angiogenesis, as well as those that are down-regulated (i.e. expressed at a lower level). In a preferred embodiment, the angiogenesis sequences are from humans; however, as

will be appreciated by those in the art, angiogenesis sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other angiogenesis sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). Angiogenesis sequences from other organisms may be obtained using the techniques outlined below.

Angiogenesis sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the angiogenesis sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of an angiogenesis protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the angiogenesis sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, angiogenesis sequences are useful in a variety of

applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the angiogenesis sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (Tm) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in Tm for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

An angiogenesis sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

The angiogenesis screen included comparing genes identified in an *in vitro* model of angiogenesis as described in Hiraoka, Cell 95:365 (1998), which is expressly incorporated by reference, with genes identified in controls. Samples of normal tissue and tissue undergoing angiogenesis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the angiogenesis screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, angiogenesis sequences are those that are up-regulated in angiogenesis disorders; that is, the expression of these genes is higher in the disease tissue as compared to normal tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and http://www.ncbi.nlm.nih.gov/. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

In a preferred embodiment, angiogenesis sequences are those that are down-regulated in the angiogenesis disorder; that is, the expression of these genes is lower in angiogenic tissue as compared to normal tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Angiogenesis sequences according to the invention may be classified into discrete clusters of sequences based on common expression profiles of the sequences. Expression levels of angiogenesis sequences may increase or decrease as a function of time in a manner that correlates with the induction of angiogenesis. Alternatively, expression levels of angiogenesis sequences may both increase and decrease as a function of time. For example, expression levels of some angiogenesis sequences are temporarily induced or diminished during the switch to the angiogenesis phenotype, followed by a return to baseline expression levels. Table 1 depicts 1774 genes, the expression of which varies as a function of time in angiogenesis tissue when compared to normal tissue. Figure 1 depicts 4 discrete expression profiles of angiogenesis genes identified in Table 1.

A particularly preferred embodiment includes the sequences as described in Table 2 which depicts a preferred subset of 559 angiogenesis sequences, the expression of which is altered in angiogenesis when compared to normal tissue.

An additional embodiment includes the sequences as described in Table 3, which depicts 1916 genes including expression sequence tags (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

A preferred embodiment includes the sequences as described in Table 4 which depicts a preferred subset of 558 genes identified in Table 3 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

A particularly preferred embodiment includes the sequences as described in Table 5 which provides a preferred subset of 20 Accession numbers identified in Table 3 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

In a particularly preferred embodiment, angiogenesis sequences are those that are induced for a period of time followed by a return to the baseline levels. Sequences that are temporarily induced provide a means to target angiogenesis tissue, for example neovascularized tumors, while avoiding rapidly growing tissue that require perpetual vascularization. Such positive angiogenic factors include aFGF, bFGF, VEGF, angiogenin and the like.

Induced angiogenesis sequences also are further categorized with respect to the timing of induction. For example, some angiogenesis genes may be induced at an early time period, such as with 10 minutes of the induction of angiogenesis. Others may be induced later, such as between 5 and 60 minutes, while yet others may be induced for a time period of about two hours or more followed by a return to baseline expression levels.

In another preferred embodiment are angiogenesis sequences that are inhibited or reduced as a function of time followed by a return to "normal" expression levels. Inhibitors of angiogenesis are examples of molecules that have this expression profile. These sequences also can be further divided into groups depending on the timing of diminished expression. For example, some molecules may display reduced expression with 10 minutes of the induction of angiogenesis. Others may be diminished later, such as between 5 and 60 minutes, while others may be diminished for a time period of about two hours or more followed by a return to baseline. Examples of such negative angiogenic factors include thrombospondin and endostatin to name a few.

In yet another preferred embodiment are angiogenesis sequences that are induced for prolonged periods. These sequences are typically associated with induction of angiogenesis and may participate in induction and/or maintenance of the angiogenesis phenotype.

In another preferred embodiment are angiogenesis sequences, the expression of which is reduced or diminished for prolonged periods in angiogenic tissue. These sequences are typically angiogenesis inhibitors and their diminution is correlated with an increase in angiogenesis.

Angiogenesis proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the angiogenesis protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleos. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or disregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the angiogenesis sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For

example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for

example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Putative transmembrane angiogenesis proteins include those encoded by the sequences labeled with "Y" in the TM column depicted in Table 2.

Angiogenesis proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the angiogenesis proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Angiogenesis proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

Putative secreted angiogenesis proteins include those encoded by the sequences depicted in Table 2 that are labeled with "Y" in the SS column, but a "N" in the TM column.

An angiogenesis sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

As used herein, a nucleic acid is an "angiogenesis nucleic acid" if the overall homology of the nucleic acid sequence to one of the nucleic acids of Table 1, Table 2, Table 3, Table 4 or Table 5 is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorith of Needleman & Wunsch, J. Mol. Biool. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the tables and figures, preferable those represented in Table 4, more preferably those represented in table 5, still more preferably those of Figures 2, 3, 7, 11, 12, 17, 21, 23 and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the tables and figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the tables and figures. In another embodiment, the sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); http://blast.wustl]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2

parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the nucleic acids of the figures. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acids identified in the figures, or their complements, are considered an angiogenesis sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al., both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH

7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, supra, and Tijssen, supra.

In addition, the angiogenesis nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the angiogenesis genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., supra, hereby expressly incorporated by reference.

Once the angiogenesis nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire angiogenesis nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant angiogenesis nucleic acid can be further-used as a probe to identify and isolate other angiogenesis nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant angiogenesis nucleic acids and proteins.

The angiogenesis nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the angiogenesis nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene therapy and/or antisense applications. Alternatively, the angiogenesis nucleic acids that include coding regions of angiogenesis proteins can be put into expression vectors for the expression of angiogenesis proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to angiogenesis nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the angiogenesis nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect;

there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluorescese. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, angiogenesis nucleic acids encoding angiogenesis proteins are used to make a variety of expression vectors to express angiogenesis proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the angiogenesis protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid

will generally be appropriate to the host cell used to express the angiogenesis protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the angiogenesis protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The angiogenesis proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an angiogenesis protein, under the appropriate conditions to induce or cause expression of the angiogenesis protein. The conditions appropriate for angiogenesis protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the

harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melangaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells),THP1 cells (a macrophage cell line) and human cells and lines.

In a preferred embodiment, the angiogenesis proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlytion signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, angiogenesis proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the angiogenesis protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located

between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, angiogenesis proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, angiogenesis protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The angiogenesis protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the angiogenesis protein may be fused to a carrier protein to form an immunogen. Alternatively, the angiogenesis protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the angiogenesis protein is an angiogenesis peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the angiogenesis nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the angiogenesis nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as $^{3}H$, $^{14}C$, $^{32}P$, $^{35}S$, or $^{125}I$, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-

galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides angiogenesis protein sequences. An angiogenesis protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the angiogenesis protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of angiogenesis proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

Angiogenesis proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of angiogenesis proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the angiogenesis nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the angiogenesis proteins are derivative or variant angiogenesis proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative

angiogenesis peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the angiogenesis peptide.

Also included within one embodiment of angiogenesis proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the angiogenesis protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant angiogenesis protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the angiogenesis protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed angiogenesis variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of angiogenesis protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the angiogenesis protein are desired, substitutions are generally made in accordance with the following chart:

Chart I

| Original Residue | Exemplary Substitutions |
|---|---|
| Ala | Ser |
| Arg | Lys |
| Asn | Gln, His |
| Asp | Glu |
| Cys | Ser |
| Gln | Asn |
| Glu | Asp |
| Gly | Pro |
| His | Asn, Gln |
| Ile | Leu, Val |
| Leu | Ile, Val |
| Lys | Arg, Gln, Glu |
| Met | Leu, Ile |
| Phe | Met, Leu, Tyr |
| Ser | Thr |
| Thr | Ser |
| Trp | Tyr |
| Tyr | Trp, Phe |
| Val | Ile, Leu |

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the angiogenesis proteins as needed. Alternatively, the variant may be designed such that the biological activity of the angiogenesis protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of angiogenesis polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an angiogenesis

polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an angiogenesis polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking angiogenesis polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-angiogenesis polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the angiogenesis polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence angiogenesis polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence angiogenesis polypeptide.

Addition of glycosylation sites to angiogenesis polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence angiogenesis polypeptide (for O-linked glycosylation sites). The angiogenesis amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the angiogenesis polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the angiogenesis polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the angiogenesis polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of angiogenesis comprises linking the angiogenesis polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Angiogenesis polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising an angiogenesis polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an angiogenesis polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the angiogenesis polypeptide. The presence of such epitope-tagged forms of an angiogenesis polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the angiogenesis polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an angiogenesis polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6**397 (1990)].

Also included with an embodiment of angiogenesis protein are other angiogenesis proteins of the angiogenesis family, and angiogenesis proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related angiogenesis proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the angiogenesis nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, angiogenesis proteins can be made that are longer than those encoded by the nucleic acids of the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Angiogenesis proteins may also be identified as being encoded by angiogenesis nucleic acids. Thus, angiogenesis proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the angiogenesis protein is to be used to generate antibodies, for example for immunotherapy, the angiogenesis protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller angiogenesis protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from AAA4p1 and AAA4p2. In another preferred embodiment the epitope is selected from AAA1p1 and AAA1p2. In another preferred embodiment the epitope is selected from AAA7p1, AAA7p2, AAA7p3 and AAA7p1m.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, $Fab_2$, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired,

an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a protein encoded by a nucleic acid of figure 1 or 3-6 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to angiogenesis protein are capable of reducing or eliminating the biological function of angiogenesis protein, as is described below. That is, the addition of anti-angiogenesis protein antibodies (either polyclonal or preferably monoclonal) to angiogenic tissue (or cells containing angiogenesis) may reduce or eliminate the angiogenesis activity. Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the angiogenesis proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some

CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of angiogenesis with an antibody raised against angiogenesis proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the angiogenesis proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted angiogenesis protein.

In another preferred embodiment, the angiogenesis protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the angiogenesis protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the

transmembrane angiogenesis protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the angiogenesis protein. The antibody is also an antagonist of the angiogenesis protein. Further, the antibody prevents activation of the transmembrane angiogenesis protein. In one aspect, when the antibody prevents the binding of other molecules to the angiogenesis protein, the antibody prevents growth of the cell. The antibody also sensitizes the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, angiogenesis is treated by administering to a patient antibodies directed against the transmembrane angiogenesis protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the angiogenesis protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the angiogenesis protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with angiogenesis.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to angiogenesis tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with angiogenesis. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diptheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against angiogenesis proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane angiogenesis proteins not only serves to increase the local concentration of therapeutic moiety in the angiogenesis afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the angiogenesis protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the

angiogenesis protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The angiogenesis antibodies of the invention specifically bind to angiogenesis proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least $10^{-4}$- $10^{-6}$ $M^{-1}$, with a preferred range being $10^{-7}$ - $10^{-9}$ $M^{-1}$.

In a preferred embodiment, the angiogenesis protein is purified or isolated after expression. Angiogenesis proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the angiogenesis protein may be purified using a standard anti-angiogenesis protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the angiogenesis protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the angiogenesis proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the angiogenesis phenotype; that is, the expression levels of genes in normal tissue (i.e. not undergoing angiogenesis) and in angiogenesis tissue (and in some cases, for varying severities of angiogenesis that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or angiogenesis tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered,

including an activation or inactivation, in, for example, normal versus angiogenic tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the angiogenesis protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to angiogenesis genes, i.e. those identified as being important in an angiogenesis phenotype, can be evaluated in an angiogenesis diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the angiogenesis protein are detected. Although DNA or RNA encoding the angiogenesis protein may be detected, of particular interest are methods wherein the mRNA encoding an angiogenesis protein is detected. The presence of mRNA in a

sample is an indication that the angiogenesis gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an angiogenesis protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, angiogenesis proteins, including intracellular, transmembrane or secreted proteins, find use as markers of angiogenesis. Detection of these proteins in putative angiogenesis tissue or patients allows for a determination or diagnosis of angiogenesis. Numerous methods known to those of ordinary skill in the art find use in detecting angiogenesis. In one embodiment, antibodies are used to detect angiogenesis proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the angiogenesis protein is detected by immunoblotting with antibodies raised against the angiogenesis protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the angiogenesis protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the angiogenesis

protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the angiogenesis protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of angiogenesis proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing angiogenesis from blood samples. As previously described, certain angiogenesis proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted angiogenesis proteins. Antibodies can be used to detect the angiogenesis by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, in situ hybridization of labeled angiogenesis nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including angiogenesis tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to angiogenesis severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the angiogenesis probes are attached to biochips for the detection and quantification of angiogenesis sequences in a tissue or patient. The assays proceed as outlined above for diagnosis.

In a preferred embodiment any of the three classes of proteins as described herein are used in drug screening assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified angiogenesis proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the angiogenesis phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in angiogenesis, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing angiogenesis, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in angiogenic tissue compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in angiogenic tissue compared to normal tissue gives a 10 fold increase in expression for a candidate agent being desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the angiogenesis protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates angiogenesis, modulates angiogenesis proteins, binds to an angiogenesis protein, or interferes between the binding of an angiogenesis protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the angiogenesis phenotype or the expression of an angiogenesis sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses an angiogenesis phenotype, for example to a normal tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe angiogenesis phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of an angiogenesis protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the

formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin.

For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

The screens are done to identify drugs or bioactive agents that modulate the angiogenesis phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in angiogenesis similar to the expression profile of normal tissue is expected to result in a suppression of the angiogenesis phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the angiogenesis phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress an angiogenesis expression pattern leading to a normal expression pattern, or modulate a single angiogenesis gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated angiogenesis tissue reveals genes that are not expressed in normal tissue or angiogenesis tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for angiogenesis genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated angiogenesis tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of angiogenic cells, that thus has an associated angiogenesis expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, angiogenesis tissue may be screened for agents that reduce or suppress the angiogenesis phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on angiogenesis activity. By defining such a signature for the angiogenesis phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "angiogenesis proteins". In preferred embodiments the angiogenesis protein is as depicted in Figures 4, 8, 13, 18, and 22 or encoded by the sequences shown in figures 2, 3, 7, 12, 17, 21 and 23. The angiogenesis protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

Preferably, the angiogenesis protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

In a preferred embodiment, the fragment is from AAA1. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the AAA1 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from AAA1p1 and AAA1p2.

In a preferred embodiment, the fragment is charged and from the c-terminus of AAA4. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In one embodiment the fragment is an internal peptide overlapping hydrophilic stretch of AAA4. In a preferred embodiment, the termini is blocked. Preferably, the fragment of AAA4 is selected from AAA4p1 or AAA4p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

In one embodiment the angiogenesis proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the angiogenesis protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the angiogenesis proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an angiogenesis protein and a candidate bioactive agent, and determining the binding of the candidate agent to the angiogenesis protein. Preferred embodiments utilize the human angiogenesis protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative angiogenesis proteins may be used.

Generally, in a preferred embodiment of the methods herein, the angiogenesis protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the angiogenesis protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the angiogenesis protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the angiogenesis protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labelled, and binding determined directly. For example, this may be done by attaching all or a portion of the angiogenesis protein to a solid support, adding a labelled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as

magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using $^{125}I$, or with fluorophores. Alternatively, more than one component may be labeled with different labels; using $^{125}I$ for the proteins, for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. angiogenesis), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the angiogenesis protein and thus is capable of binding to, and potentially modulating, the activity of the angiogenesis protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the angiogenesis protein with a higher affinity. Thus, if the candidate

bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the angiogenesis protein.

In a preferred embodiment, the methods comprise differential screening to identity bioactive agents that are capable of modulating the activitity of the angiogenesis proteins. In this embodiment, the methods comprise combining an angiogenesis protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, an angiogenesis protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the angiogenesis protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the angiogenesis protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native angiogenesis protein, but cannot bind to modified angiogenesis proteins. The structure of the angiogenesis protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect angiogenesis bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of angiogenesis proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of angiogenesis proteins comprise the steps of adding a candidate bioactive agent to a sample of angiogenesis proteins, as above, and determining an alteration in the biological activity of

angiogenesis proteins. "Modulating the activity of angiogenesis proteins" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to angiogenesis proteins(although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of angiogenesis proteins.

Thus, in this embodiment, the methods comprise combining an angiogenesis sample and a candidate bioactive agent, and evaluating the effect on angiogenesis. By "angiogenesis activity" or grammatical equivalents herein is meant one of angiogenesis's biological activities, including, but not limited to, its role in angiogenesis. In one embodiment, angiogenesis activity includes activation of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10. An inhibitor of angiogenesis activity is the inhibition of any one or more angiogenesis activities.

In a preferred embodiment, the activity of the angiogenesis protein is increased; in another preferred embodiment, the activity of the angiogenesis protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of an angiogenesis protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising angiogenesis proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an angiogenesis protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the angiogenesis protein. In one embodiment, "angiogenesis protein activity" as used herein includes at least one of the following: angiogenesis protein activity as defined herein, binding to Edg-1, activation of Edg-1, or activation of substrates of Edg-1. In one embodiment, angiogenesis activity is defined as the unregulated proliferation of angiogenic tissue, or

the growth of arteries in tissue. In one aspect, angiogenesis activity as defined herein is related to the activity of Edg-1 in the upregulation of Edg-1 in angiogenic tissue.

In another embodiment, angiogenesis protein activity includes at least one of the following: angiogenesis activity, binding to one of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, or activation of substrates of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, respectively. In one preferred embodiment, AAA1 comprises its N-terminal end. In one aspect, angiogenesis activity as defined herein is related to the activity of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, in the upregulation of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, respectively in angiogenesis tissue.

In one embodiment, a method of inhibiting angiogenic cell division is provided. The method comprises administration of a angiogenesis inhibitor.

In another embodiment, a method of inhibiting angiogenesis is provided. The method comprises administration of an angiogenesis inhibitor.

In a further embodiment, methods of treating cells or individuals with angiogenesis are provided. The method comprises administration of an angiogenesis inhibitor.

In one embodiment, an angiogenesis inhibitor is an antibody as discussed above. In another embodiment, the angiogenesis inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for angiogenesis molecules. A preferred antisense molecule is for AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, or matrix metalloproteinase 10, more preferable the angiogenesis sequences in Table 5, or for a ligand or activator thereof. A most preferred antisense molecule is for Edg-1 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable

ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various angiogenesis sequences are important in angiogenesis. Accordingly, disorders based on mutant or variant angiogenesis genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant angiogenesis genes comprising determining all or part of the sequence of at least one endogeneous angiogenesis genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the angiogenesis genotype of an individual comprising determining all or part of the sequence of at least one angiogenesis gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced angiogenesis gene to a known angiogenesis gene, i.e. a wild-type gene.

The sequence of all or part of the angiogenesis gene can then be compared to the sequence of a known angiogenesis gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a a difference in the sequence between the angiogenesis gene of the patient and the known angiogenesis gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the angiogenesis genes are used as probes to determine the number of copies of the angiogenesis gene in the genome.

In another preferred embodiment, the angiogenesis genes are used as probes to determine the chromosomal localization of the angiogenesis genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the angiogenesis gene locus.

Thus, in one embodiment, methods of modulating angiogenesis in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-angiogenesis antibody that reduces or eliminates the biological activity of an endogeneous angiogenesis protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding an angiogenesis protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the angiogenesis sequence is down-regulated in angiogenesis, the activity of the angiogenesis gene is increased by increasing the amount of angiogenesis in the cell, for example by overexpressing the endogeneous angiogenesis or by administering a gene encoding the angiogenesis sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entireity. Alternatively, for example when the angiogenesis sequence is up-regulated in angiogenesis, the activity of the endogeneous angiogenesis gene is decreased, for example by the administration of a angiogenesis antisense nucleic acid.

In one embodiment, the angiogenesis proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to angiogenesis proteins, which are useful as described herein. Similarly, the angiogenesis proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify angiogenesis antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a angiogenesis protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a

number of applications. For example, the angiogenesis antibodies may be coupled to standard affinity chromatography columns and used to purify angiogenesis proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the angiogenesis protein.

In one embodiment, a therapeutically effective dose of an angiogenesis proteins and modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for angiogenesis degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

The administration of the angiogenesis proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the angiogenesis proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise an angiogenesis protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as

sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, angiogenesis proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, angiogenesis genes (including both the full-length sequence, partial sequences, or regulatory sequences of the angiogenesis coding regions) can be administered in gene therapy applications, as is known in the art. These angiogenesis genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

In a preferred embodiment, angiogenesis genes are administered as DNA vaccines, either single genes or combinations of angiogenesis genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

In one embodiment, angiogenesis genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing an angiogenesis gene or portion of an angiogenesis gene under the control of a promoter for expression in an angiogenesis patient. The angiogenesis gene used for DNA vaccines can encode full-length angiogenesis proteins, but more preferably encodes portions of the angiogenesis proteins including peptides derived from the angiogenesis protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an angiogenesis gene. Similarly, it is possible to immunize a patient with a plurality of angiogenesis genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing angiogenesis proteins.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the angiogenesis polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

In another preferred embodiment angiogenesis genes find use in generating animal models of angiogenesis. As is appreciated by one of ordinary skill in the art, when the angiogenesis gene identified is repressed or diminished in angiogenesis tissue, gene therapy technology wherein antisense RNA directed to the angiogenesis gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of angiogenesis that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the angiogenesis protein. When desired, tissue-specific expression or knockout of the angiogenesis protein may be necessary.

It is also possible that the angiogenesis protein is overexpressed in angiogenesis. As such, transgenic animals can be generated that overexpress the angiogenesis protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of angiogenesis and are additionally useful in screening for bioactive molecules to treat angiogenesis.

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

## EXAMPLES

### Example 1

### Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIzol Reagent

Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A

generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

HOMOGENIZATION

Before using generator, it should have been cleaned after last usage by running it through soapy H20 and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.

Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.
Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.
Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.
Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

RNA PRECIPITATION

Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

RNA WASH

Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C.
Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried

leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC $H_20$. Try for 2-5ug/ul. Take absorbance readings.

Purify poly A+ mRNA from total RNA or clean up total RNA with Qiagen' s RNeasy kit

Purification of poly A$^+$ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A$^+$ mRNA has occurred.

Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated.
Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

Ethanol Precipitation

Add 0.4 vol. of 7.5 M $NH_4OAc$ + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash

pellet with 0.5ml of 80%ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood. (Do not speed vacuum). Suspend pellet in DEPC $H_20$ at 1ug/ul concentration.

Clean up total RNA using Qiagen's RNeasy kit

Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

First Strand cDNA Synthesis

Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT Incubate at 37C for 1 hour.

Second Strand Synthesis

Place 1st strand reactions on ice.

Add: 91ul DEPC H20
30ul 5X 2nd Strand Buffer
3ul 10mM dNTP mix
1ul 10U/ul *E.coli* DNA Ligase
4ul 10U/ul *E.coli* DNA Polymerase
1ul 2U/ul RNase H

Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C.

Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes: Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH4Oac and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

Make NTP labeling mix:

| | | |
|---|---|---|
| Combine at room temperature: | 2ul | T7 10xATP (75mM) (Ambion) |
| | 2ul | T7 10xGTP (75mM) (Ambion) |
| | 1.5ul | T7 10xCTP (75mM) (Ambion) |
| | 1.5ul | T7 10xUTP (75mM) (Ambion) |
| | 3.75ul | 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo) |
| | 3.75ul | 10mM Bio-16-CTP (Enzo) |
| | 2ul | 10x T7 transcription buffer (Ambion) |
| | 2ul | 10x T7 enzyme mix (Ambion) |

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:
200 mM Tris-acetate, pH 8.1
500 mM KOAc
150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization
200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

Hybrization Mix: fragment labeled RNA (50ng/ul final conc.)
50 pM 948-b control oligo
1.5 pM BioB
5 pM BioC
25 pM BioD
100 pM CRE
0.1mg/ml herring sperm DNA
0.5mg/ml acetylated BSA
to 300 ul with 1xMES hyb. buffer

The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:
Start with non-biotinylated IVT (purified by RNeasy columns)
(see example 1 for steps from tissue to IVT)
IVT antisense RNA; 4 µg: µl

Random Hexamers (1 µg/µl): 4 µl
$H_2O$: µl

14 µl

- Incubate 70°C, 10 min. Put on ice.

Reverse transcription:
5X First Strand (BRL) buffer: 6 µl
0.1 M DTT: 3 µl
50X dNTP mix: 0.6 µl
H2O: 2.4 µl
Cy3 or Cy5 dUTP (1mM): 3 µl
SS RT II (BRL): 1 µl

16 µl

- Add to hybridization reaction.
- Incubate 30 min., 42°C.
- Add 1 µl SSII and let go for another hour.
Put on ice.
- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H2O. dNTPs from Pharmacia)

RNA degradation:

- Add 1.5 µl 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min. 86 µl $H_2O$, 10 µl 10N NaOH, 4 µl 50mM EDTA

U-Con 30
500 µl TE/sample spin at 7000g for 10 min, save flow through for purification

Qiagen purification:
-suspend u-con recovered material in 500µl buffer PB
-proceed w/ normal Qiagen protocol

DNAse digest:
- Add 1 µl of 1/100 dil of DNAse/30µl Rx and incubate at 37°C for 15 min.
-5 min 95°C to denature enzyme

Sample preparation:

- Add:

| | |
|---|---|
| Cot-1 DNA: 10 µl | |
| 50X dNTPs: 1 µl | |
| 20X SSC: 2.3 µl | |
| Na pyro phosphate: 7.5 µl | |
| 10mg/ml Herring sperm DNA | 1ul of 1/10 dilution |
| | 21.8 final vol. |

- Dry down in speed vac.
- Resuspend in 15 µl $H_20$.
- Add 0.38 µl 10% SDS.
- Heat 95°C, 2 min.
- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

Washing after the hybridization:

| | |
|---|---|
| 3X SSC/0.03% SDS: | 2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls $H_2O$ |
| 1X SSC: 5 min. | 12.5 mls 20X SSC in 250mls $H_2O$ |
| 0.2X SSC: 5 min. | 2.5 mls 20X SSC in 250mls $H_2O$ |

Dry slides in centrifuge, 1000 RPM, 1min.

Scan at appropiate PMT's and channels.

The results are shown in the tables and figures. The lists of genes come from cells cultured in an in vitro angiogenesis model. As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length.

TABLE 1

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 3 | AB000450 | vaccinia related kinase 2 |
| 4 | AB002380 | Human mRNA for KIAA382 gene; partial cds |
| 4 | AB003103 | proteasome (prosome; macropain) 26S subunit; non-ATPase; 12 |
| 4 | AB004884 | Homo sapiens mRNA for PKU-alpha; partial cds |
| 1 | AF000573_ma1 | homogentisate 1;2-dioxygenase (homogentisate oxidase) |
| 3 | AF008937 | Homo sapiens syntaxin-16C mRNA, complete cds |
| 3 | AF009301 | Homo sapiens TEB4 protein mRNA; complete cds |
| 3 | AF009368 | Homo sapiens Luman mRNA; complete cds |
| 4 | D00591 | chromosome condensation 1 |
| 4 | D00760 | proteasome (prosome; macropain) subunit; alpha type; 2 |
| 1 | D11139 | tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity; collagenase inhibitor) |
| 4 | D14657 | Human mRNA for KIAA11 gene; complete cds |
| 4 | D14878 | D123 gene product |
| 1 | D17716 | mannosyl (alpha-1;6-)-glycoprotein beta-1;6-N-acetyl-glucosaminyltransferase |
| 4 | D21090 | RAD23 (S. cerevisiae) homolog B |
| 1 | D26135 | diacylglycerol kinase; gamma (9kD) |
| 1 | D26528 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 7 (RNA helicase; 52kD) |
| 1 | D30742 | calcium/calmodulin-dependent protein kinase IV |
| 4 | D31762 | Human mRNA for KIAA57 gene; complete cds |
| 4 | D31765 | Human mRNA for KIAA61 gene; partial cds |
| 3 | D31888 | Homo sapiens clone 2479 mRNA sequence |
| 4 | D38128 | prostaglandin I2 (prostacyclin) receptor (IP) |
| 2 | D38500 | postmeiotic segregation increased 2-like 4 |
| 4 | D38551 | RAD21 (S. pombe) homolog |
| 4 | D42087 | Human mRNA for KIAA118 gene; partial cds |
| 3 | D49396 | Human mRNA for Apo1_Human (MER5(Aop1-Mouse)-like protein); complete cds |
| 4 | D55640 | Human monocyte PABL (pseudoautosomal boundary-like sequence) mRNA, clone Mo2 |
| 1 | D63391 | platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD) |
| 3 | D63477 | Human mRNA for KIAA143 gene; partial cds |
| 4 | D63483 | acetyl LDL receptor; SREC |
| 4 | D64015 | TIA1 cytotoxic granule-associated RNA-binding protein-like 1 |
| 4 | D79990 | Human mRNA for KIAA168 gene; complete cds |
| 4 | D79997 | Human mRNA for KIAA175 gene; complete cds |
| 4 | D80010 | Human mRNA for KIAA188 gene; partial cds |
| 1 | D84276 | CD38 antigen (p45) |
| 4 | D86425 | Homo sapiens mRNA for nidogen-2 |
| 4 | D86978 | Human mRNA for KIAA225 gene; partial cds |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 1 | D87012 | Homo sapiens clone 24675 mRNA sequence |
| 4 | D87075 | Human mRNA for KIAA238 gene; partial cds |
| 4 | D87432 | solute carrier family 7 (cationic amino acid transporter; y+ system); |
| 4 | D87448 | Homo sapiens mRNA for DNA topoisomerase II binding protein; complete cds |
| 2 | D87845 | platelet-activating factor acetylhydrolase 2 (4kD) |
| 1 | HG1098-HT1098 | Cystatin D |
| 4 | HG2167-HT2237 | Protein Kinase Ht31, Camp-Dependent |
| 1 | HG2415-HT2511 | Transcription Factor E2f-2 |
| 1 | HG2825-HT2949 | Ret Transforming Gene |
| 1 | HG2887-HT3031_r | Sry-Related Hmg-Box 12 Protein (Gb:X73039) |
| 4 | HG4660-HT5073 | Microtubule-Associated Protein 1b |
| 3 | HG4704-HT5146 | Glial Growth Factor 2 |
| 4 | HG884-HT884 | Oncogene E6-Ap, Papillomavirus |
| 1 | HG919-HT919 | Dna Polymerase, Epsilon, Catalytic Subunit |
| 4 | J00212_f | Accession not listed in Genbank |
| 4 | J04029 | keratin 1 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) |
| 4 | J04031 | 5;1-methylenetetrahydrofolate dehydrogenase; 5;1-methylenetetrahydrofolate cyclohydrolase; 1-formyltetrahydrofolate synthetase |
| 4 | J04088 | topoisomerase (DNA) II alpha (17kD) |
| 4 | J04543 | annexin VII (synexin) |
| 4 | L06139 | TEK tyrosine kinase; endothelial |
| 1 | L07540 | ACTIVATOR 1 36 KD SUBUNIT |
| 4 | L08895 | MADS box transcription enhancer factor 2; polypeptide C (myocyte enhancer factor 2C) |
| 1 | L11239 | gastrulation brain homeo box 1 |
| 1 | L11353 | neurofibromin 2 (bilateral acoustic neuroma) |
| 4 | L13773 | Human AF-4 mRNA; complete cds |
| 4 | L13800 | Homo sapiens liver expressed protein gene, 3' end |
| 4 | L14922 | replication factor C (activator 1) 1 (145kD) |
| 4 | L15189 | heat shock 7kD protein 9B (mortalin-2) |
| 4 | L15388 | Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds |
| 3 | L16895 | lysyl oxidase |
| 4 | L27476 | Friedreich ataxia region gene X14 (tight junction protein ZO-2) |
| 4 | L27624 | TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR |
| 1 | L32976 | mixed lineage kinase 3 |
| 1 | L33404 | protease; serine; 6 (chymotryptic; stratum corneum) |
| 4 | L35263 | cytokine suppressive anti-inflammatory drug binding protein 1 (p38 MAP kinase) |
| 1 | L37347 | natural resistance-associated macrophage protein 2 |
| 4 | L40371 | thyroid hormone receptor interactor 4 |
| 4 | L40391 | Homo sapiens (clone s153) mRNA fragment |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 4 | L41607 | glucosaminyl (N-acetyl) transferase 2; I-branching enzyme |
| 1 | L77566 | Homo sapiens DGS-I mRNA; 3' end |
| 1 | M13928 | aminolevulinate; delta-; dehydratase |
| 1 | M14016 | uroporphyrinogen decarboxylase |
| 4 | M14219 | decorin |
| 4 | M15796 | proliferating cell nuclear antigen |
| 4 | M21305 | Human alpha satellite and satellite 3 junction DNA sequence |
| 4 | M22092 | Human neural cell adhesion molecule (N-CAM) gene, exon SEC and partial cds |
| 4 | M22898 | tumor protein p53 (Li-Fraumeni syndrome) |
| 3 | M22995 | RAP1A; member of RAS oncogene family |
| 3 | M23379 | RAS p21 protein activator (GTPase activating protein) 1 |
| 1 | M24364 | major histocompatibility complex; class II; DQ beta 1 |
| 1 | M24400 | chymotrypsinogen B1 |
| 3 | M25753 | cyclin B1 |
| 4 | M27691 | cAMP responsive element binding protein 1 |
| 4 | M28213 | RAB2; member RAS oncogene family |
| 4 | M29550 | SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT; BETA ISOFORM |
| 1 | M29971 | O-6-methylguanine-DNA methyltransferase |
| 4 | M30269 | nidogen (enactin) |
| 4 | M31158 | protein kinase; cAMP-dependent; regulatory; type II; beta |
| 3 | M31166 | pentaxin-related gene; rapidly induced by IL-1 beta |
| 3 | M31210 | endothelial differentiation; sphingolipid G-protein-coupled receptor; 1 |
| 1 | M55420 | Human IgE chain, last 2 exons |
| 4 | M59979 | prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) |
| 4 | M62810 | transcription factor 6-like 1 (mitochondrial transcription factor 1-like) |
| 4 | M63838 | interferon; gamma-inducible protein 16 |
| 1 | M64710 | Human C-type natriuretic peptide gene, complete cds |
| 3 | M68874 | Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds |
| 3 | M74524 | ubiquitin-conjugating enzyme E2A (RAD6 homolog) |
| 1 | M80254 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; MITOCHONDRIAL PRECURSOR |
| 1 | M81780_cds3 | sphingomyelin phosphodiesterase 1; acid lysosomal (acid sphingomyelinase) |
| 4 | M83822 | Human beige-like protein (BGL) mRNA; partial cds |
| 4 | M86934 | GS1 PROTEIN |
| 1 | M87338 | replication factor C (activator 1) 2 (4kD) |
| 1 | M96326_ma1 | azurocidin 1 (cationic antimicrobial protein 37) |
| 4 | M96954 | TIA1 cytotoxic granule-associated RNA-binding protein-like 1 |
| 4 | M98833 | Friend leukemia virus integration 1 |
| 1 | S66793 | arrestin 3; retinal (X-arrestin) |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 1 | S72370 | pyruvate carboxylase |
| 4 | S78569 | laminin; alpha 4 |
| 4 | S79873 | lysosomal-associated membrane protein 2 |
| 1 | S83325 | aspartate beta-hydroxylase |
| 4 | S83364 | putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, mRNA Partial, 366 nt] |
| 1 | S83365 | putative Rab5-interacting protein (clone L1-94) [human, HeLa cells, mRNA Partial, 369 nt] |
| 1 | U01212 | Human olfactory marker protein (OMP) gene, complete cds |
| 1 | U01922 | deafness; X-linked 1; progressive |
| 4 | U02556 | Human RP3 mRNA; complete cds |
| 4 | U02680 | protein tyrosine kinase 9 |
| 4 | U03272 | fibrillin 2 |
| 4 | U04209 | Human associated microfibrillar protein mRNA; complete cds |
| 4 | U05237 | fetal Alzheimer antigen |
| 1 | U07225 | purinergic receptor P2Y; G-protein coupled; 2 |
| 3 | U07620 | protein kinase mitogen-activated 1 (MAP kinase) |
| 4 | U09759 | protein kinase mitogen-activated 9 (MAP kinase) |
| 4 | U09820 | alpha thalassemia/mental retardation syndrome X-linked |
| 3 | U11313 | sterol carrier protein 2 |
| 3 | U14518 | centromere protein A (17kD) |
| 4 | U14575 | protein phosphatase 1; regulatory (inhibitor) subunit 8 |
| 3 | U15173 | BCL2/adenovirus E1B 19kD-interacting protein 2 |
| 4 | U15932 | dual specificity phosphatase 5 |
| 4 | U18291 | cell division cycle 16; anaphase promoting complex 6 |
| 4 | U18300 | damage-specific DNA binding protein 2 (48kD) |
| 4 | U18383 | nuclear respiratory factor 1 |
| 4 | U20536 | caspase 6; apoptosis-related cysteine protease |
| 4 | U21551 | Human ECA39 mRNA; complete cds |
| 4 | U23028 | eukaryotic translation initiation factor 2B; subunit 5 (epsilon; 82kD) |
| 1 | U23752 | SRY (sex-determining region Y)-box 11 |
| 4 | U25435 | Human transcriptional repressor (CTCF) mRNA; complete cds |
| 4 | U25997 | stanniocalcin |
| 4 | U28251_cds2 | zinc finger protein 169 |
| 4 | U28831 | Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA; partial cds |
| 4 | U30245 | Human myelomonocytic specific protein (MNDA) gene, 5' flanking sequence and complete exon 1 |
| 4 | U32315 | Human syntaxin 3 mRNA; complete cds |
| 4 | U32439 | regulator of G-protein signalling 7 |
| 3 | U32849 | N-myc (and STAT) interactor |
| 4 | U35139 | necdin (mouse) homolog |
| 1 | U36764 | eukaryotic translation initiation factor 3; subunit 2 (beta; 36kD) |
| 4 | U39400 | chromosome 11 open reading frame 4 |
| 4 | U39657 | protein kinase; mitogen-activated; kinase 6 (MAP kinase kinase 6) |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 4 | U41344 | proline arginine-rich end leucine-rich repeat protein |
| 3 | U41766 | a disintegrin and metalloproteinase domain 9 (meltrin gamma) |
| 3 | U41813 | homeo box A9 |
| 3 | U41815 | Human nucleoporin 98 (NUP98) mRNA, complete cds |
| 4 | U43286 | Human selenophosphate synthetase 2 (SPS2) mRNA; complete cds |
| 4 | U44378 | MAD (mothers against decapentaplegic; Drosophila) homolog 4 |
| 4 | U44754 | small nuclear RNA activating complex; polypeptide 1; 43kD |
| 1 | U47011_cds1 | fibroblast growth factor 8 (androgen-induced) |
| 4 | U47077 | Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA; complete cds |
| 4 | U48251 | Homo sapiens protein kinase C-binding protein RACK7 mRNA; partial cds |
| 4 | U50535 | Human BRCA2 region; mRNA sequence CG6 |
| 4 | U56833 | von Hippel-Lindau binding protein 1 |
| 4 | U58091 | cullin 4B |
| 1 | U58837 | cyclic nucleotide gated channel beta 1 |
| 4 | U59289 | cadherin 13; H-cadherin (heart) |
| 4 | U59863 | TNF receptor-associated factor 2 |
| 4 | U67122 | ubiquitin-like 1 (sentrin) |
| 4 | U67319 | caspase 7; apoptosis-related cysteine protease |
| 3 | U68019 | MAD (mothers against decapentaplegic; Drosophila) homolog 3 |
| 1 | U69611 | a disintegrin and metalloproteinase domain 17 (tumor necrosis factor; alpha; converting enzyme) |
| 4 | U70322 | karyopherin (importin) beta 2 |
| 4 | U73524 | Human putative ATP/GTP-binding protein (HEAB) mRNA; complete cds |
| 4 | U79267 | Human clone 2384 mRNA; partial cds |
| 4 | U79291 | Human clone 23721 mRNA sequence |
| 4 | U82671_cds2 | Homo sapiens clone LM1955 H15e3 gene; partial cds |
| 4 | U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 |
| 4 | U90914 | carboxypeptidase D |
| 1 | U91316 | Homo sapiens mRNA for brain acyl-CoA hydrolase; complete cds |
| 4 | U91932 | clathrin-associated/assembly/adaptor protein; small 3; 22-kD; Sigma3A |
| 4 | U96131 | Homo sapiens HPV16 E1 protein binding protein mRNA; complete cds |
| 4 | U97018 | echinoderm microtubule-associated protein-like |
| 4 | U97188 | Homo sapiens putative RNA binding protein KOC (koc) mRNA; complete cds |
| 4 | V00503 | collagen; type I; alpha 2 |
| 3 | X04327 | 2;3-bisphosphoglycerate mutase |
| 1 | X06389 | synaptophysin |
| 1 | X07496 | apolipoprotein A-I |
| 2 | X07820 | matrix metalloproteinase 1 (stromelysin 2) |
| 3 | X14787 | thrombospondin 1 |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 4 | X15525_ma1 | acid phosphatase 2; lysosomal |
| 3 | X16396 | NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE |
| 4 | X16609 | ankyrin 1; erythrocytic |
| 4 | X53586_ma1 | Human mRNA for integrin alpha 6 |
| 4 | X53793 | MULTIFUNCTIONAL PROTEIN ADE2 |
| 1 | X54936 | placental growth factor; vascular endothelial growth factor-related protein |
| 4 | X55740 | 5' nucleotidase (CD73) |
| 2 | X57025 | insulin-like growth factor 1 (somatomedin C) |
| 2 | X60673_ma1 | adenylate kinase 3 |
| 4 | X60708 | dipeptidylpeptidase IV (CD26; adenosine deaminase complexing protein 2) |
| 4 | X62048 | wee1+ (S. pombe) homolog |
| 2 | X63097 | Rhesus blood group, D antigen |
| 4 | X63563 | polymerase (RNA) II (DNA directed) polypeptide B (14kD) |
| 4 | X64037 | general transcription factor IIF; polypeptide 1 (74kD subunit) |
| 4 | X69636 | hect domain and RLD 2 |
| 4 | X69878 | fms-related tyrosine kinase 4 |
| 4 | X70649 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 |
| 3 | X72841 | H.sapiens IEF 7442 mRNA |
| 4 | X74987 | ribonuclease L (2';5'-oligoisoadenylate synthetase-dependent) inhibitor |
| 4 | X83107 | BMX non-receptor tyrosine kinase |
| 3 | X84194 | acylphosphatase 1; erythrocyte (common) type |
| 4 | X85753 | cyclin-dependent kinase 8 |
| 1 | X87870 | H.sapiens mRNA for hepatocyte nuclear factor 4a |
| 4 | X89066 | transient receptor potential channel 1 |
| 4 | X89398_cds2 | uracil-DNA glycosylase |
| 1 | X89399 | Homo sapiens mRNA for Ins(1;3;4;5)P4-binding protein |
| 3 | X89426 | H.sapiens mRNA for ESM-1 protein |
| 4 | X91247 | thioredoxin reductase 1 |
| 4 | X91648 | H.sapiens mRNA for pur alpha extended 3'untranslated region |
| 4 | X92098 | H.sapiens mRNA for transmembrane protein mp24 |
| 4 | X92110 | H.sapiens mRNA for hcgVIII protein |
| 4 | X94703 | RAB28; member RAS oncogene family |
| 1 | X96506 | H.sapiens mRNA for NC2 alpha subunit |
| 1 | X97230_f | Homo sapiens natural killer-associated transcript 5 (NKAT5) mRNA; complete cds |
| 4 | X98263 | H.sapiens mRNA for M-phase phosphoprotein; mpp6 |
| 4 | X98296 | ubiquitin specific protease 9; X chromosome (Drosophila fat facets related) |
| 4 | X99584 | H.sapiens mRNA for SMT3A protein |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 4 | Y00264 | amyloid beta (A4) precursor protein (protease nexin-II; Alzheimer disease) |
| 4 | Y07566 | H.sapiens mRNA for RIT protein |
| 3 | Y07759 | myosin VA (heavy polypeptide 12; myoxin) |
| 1 | Y07827 | Human butyrophilin (BTF5) mRNA; complete cds |
| 4 | Y07867 | pirin |
| 4 | Y09443 | alkylglycerone phosphate synthase |
| 4 | Y09858 | H.sapiens mRNA for unknown protein |
| 4 | Y12394 | karyopherin alpha 3 (importin alpha 4) |
| 3 | Z11559 | iron-responsive element binding protein 1 |
| 4 | Z11695 | protein kinase; mitogen-activated 1 (MAP kinase 1; p4; p41) |
| 3 | Z15005 | centromere protein E (312kD) |
| 1 | Z46261 | H.sapiens DNA for histone H3a |
| 2 | AA011243_s | ESTs |
| 2 | AA018418 | ESTs |
| 2 | AA018758 | ESTs |
| 2 | AA018804 | Homo sapiens clone 23675 mRNA sequence |
| 3 | AA031993 | Homo sapiens HRIHFB2115 mRNA; partial cds |
| 2 | AA044217 | ESTs; Weakly similar to similar to cuticle collagen [C.elegans] |
| 4 | AA046548 | SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1 |
| 2 | AA057447_s | ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens] |
| 2 | AA058376 | Sjogren syndrome antigen A2 (6kD; ribonucleoprotein autoantigen SS-A/Ro) |
| 4 | AA083572 | v-ral simian leukemia viral oncogene homolog A (ras related) |
| 4 | AA085696 | ESTs |
| 2 | AA088744 | ESTs |
| 2 | AA089688 | ESTs; Weakly similar to putative T1/ST2 receptor binding protein precursor [H.sapiens] |
| 4 | AA091284 | ESTs |
| 2 | AA092700 | ESTs |
| 1 | AA092968 | ESTs |
| 4 | AA094800 | eukaryotic translation initiation factor 3; subunit 7 (zeta; 66/67kD) |
| 4 | AA100219 | ESTs |
| 4 | AA114885 | ESTs |
| 4 | AA129547 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] |
| 4 | AA133016 | ESTs |
| 3 | AA149507 | homolog of mouse quaking QKI (KH domain RNA binding protein) |
| 2 | AA151005 | sperm surface protein |
| 4 | AA187101 | zp61b6.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:624659 5', mRNA sequence |
| 3 | AA195179_s | ESTs |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 2 | AA203138 | low density lipoprotein receptor (familial hypercholesterolemia) |
| 2 | AA203645 | ESTs; Moderately similar to SH3-containing protein p415 [R.norvegicus] |
| 3 | AA206236 | zq54c6.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645418 5' similar to TR:G122922 G122922 ALLOGRAFT INFLAMMATORY FACTOR-1. ;, mRNA sequence |
| 1 | AA227621 | ESTs; Weakly similar to weak similarity to collagens [C.elegans] |
| 4 | AA248283 | ESTs; Weakly similar to X-linked retinopathy protein (C-terminal; clone XEH.8c) [H.sapiens] |
| 3 | AA249611 | H.sapiens mRNA for 21-Glutamic Acid-Rich Protein (21-GARP) |
| 2 | AA282640 | ESTs |
| 2 | AA287199 | Human mRNA for KIAA81 gene; partial cds |
| 2 | AA313990 | ESTs; Highly similar to HYPOTHETICAL 3.5 KD PROTEIN C3A5.3 IN CHROMOSOME III [Caenorhabditis elegans] |
| 2 | AA314256 | EST18611 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end, mRNA sequence |
| 2 | AA314389 | ESTs; Highly similar to ADP-RIBOSYLATION FACTOR 1 [Saccharomyces cerevisiae] |
| 2 | AA324364 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 3 | AA329211_s | ESTs |
| 2 | AA399187 | ESTs |
| 4 | AA421079 | ESTs |
| 2 | AA422029 | ESTs |
| 3 | AA425230 | Human GAP SH3 binding protein mRNA; complete cds |
| 4 | AA447052 | ESTs; Highly similar to N-terminal asparagine amidohydrolase [M.musculus] |
| 4 | AA452000 | ESTs |
| 4 | AA456687 | ESTs |
| 4 | AA487015_s | ESTs; Weakly similar to X-linked retinopathy protein (C-terminal; clone XEH.8c) [H.sapiens] |
| 2 | AB002326 | Human mRNA for KIAA328 gene; partial cds |
| 4 | AFFX-BioB-3 | . |
| 2 | C01527 | ESTs |
| 4 | C01714 | Homo sapiens serum-inducible kinase mRNA; complete cds |
| 3 | C01811_f | ESTs |
| 2 | C02352_s | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] |
| 1 | C02375 | Human mRNA containing an Alu repeat and its reverse complement |
| 2 | C14448 | EST |
| 4 | D16611_s | coproporphyrinogen oxidase (coproporphyria; harderoporphyria) |
| 2 | D25216 | Human mRNA for KIAA14 gene; complete cds |
| 2 | D31352 | ESTs; Weakly similar to hypothetical protein [H.sapiens] |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 4 | D58024_s | ESTs; Weakly similar to probable hormone receptor EMR1 precursor [H.sapiens] |
| 1 | D80897 | Homo sapiens clone 24736 mRNA sequence |
| 3 | D82614 | ESTs |
| 4 | D87845 | platelet-activating factor acetylhydrolase 2 (4kD) |
| 1 | D89377_i | msh (Drosophila) homeo box homolog 2 |
| 2 | H06583 | cAMP responsive element binding protein-like 2 |
| 1 | H40732 | ESTs |
| 4 | H46617 | yp19h1.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187921 5', mRNA sequence |
| 1 | H56731 | ESTs |
| 1 | H75570 | ESTs |
| 2 | H78886 | ESTs |
| 1 | H81241 | ESTs; Highly similar to ERYTHROID KRUEPPEL-LIKE TRANSCRIPTION FACTOR [Mus musculus] |
| 1 | L36531 | integrin; alpha 8 |
| 2 | M63154 | gastric intrinsic factor (vitamin B synthesis) |
| 4 | M63180 | threonyl-tRNA synthetase |
| 2 | M91504 | ESTs |
| 2 | N56191 | Homo sapiens protocadherin 68 (PCH68) mRNA; complete cds |
| 2 | N78483 | ESTs |
| 2 | N79268 | zinc finger protein 198 |
| 2 | R14652 | Homo sapiens PAC clone DJ872F7 from 7q31 |
| 2 | R20459 | yg33f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5', mRNA sequence |
| 3 | R22303 | ESTs; Weakly similar to putative p15 [H.sapiens] |
| 2 | R33779 | ESTs; Weakly similar to p4 [H.sapiens] |
| 2 | R36553 | ESTs; Weakly similar to KIAA681 protein [H.sapiens] |
| 2 | R64534 | ESTs |
| 4 | R66475 | ESTs |
| 4 | R70621 | Homo sapiens mRNA for KIAA896 protein; partial cds |
| 3 | R79356 | ESTs; Weakly similar to PROTEIN Q3 [Mus musculus] |
| 2 | R84933 | ESTs; Weakly similar to putative p15 [H.sapiens] |
| 3 | RC_AA007160 | ESTs |
| 2 | RC_AA007234_s | ESTs; Highly similar to protein tyrosine phosphatase epsilon cytoplasmic isoform [H.sapiens] |
| 2 | RC_AA018409 | ESTs |
| 4 | RC_AA025351 | ESTs |
| 3 | RC_AA027168 | ESTs |
| 1 | RC_AA027317 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_AA029423 | ESTs |
| 4 | RC_AA031357 | ESTs |
| 4 | RC_AA045136 | ESTs |
| 1 | RC_AA053400 | ESTs |

| Cluster | Accession # PROBESET | Gene Description |
|---|---|---|
| 3 | RC_AA055829 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_AA065217 | ESTs |
| 1 | RC_AA116054 | ESTs |
| 1 | RC_AA126311 | ESTs |
| 4 | RC_AA129390 | ESTs |
| 4 | RC_AA130273 | ESTs; Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster] |
| 2 | RC_AA142919 | ESTs |
| 4 | RC_AA150205 | ubiquitous Kruppel-like transcription factor |
| 1 | RC_AA176867 | ESTs |
| 2 | RC_AA180321 | ESTs; Highly similar to U1 small nuclear ribonucleoprotein 1SNRP homolog [H.sapiens] |
| 2 | RC_AA180487 | Homo sapiens TACC1 (TACC1) mRNA; complete cds |
| 4 | RC_AA187634 | eukaryotic translation initiation factor 3; subunit 1 (alpha; 35kD) |
| 3 | RC_AA195399 | ESTs |
| 3 | RC_AA234717 | ESTs |
| 4 | RC_AA234743 | ESTs |
| 3 | RC_AA234957 | Homo sapiens mRNA for MTMR1 protein |
| 3 | RC_AA235604 | ESTs |
| 3 | RC_AA236559 | ESTs; Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58] |
| 3 | RC_AA242868 | ESTs; Weakly similar to house-keeping protein [M.musculus] |
| 4 | RC_AA251776 | jun D proto-oncogene |
| 4 | RC_AA251909 | Homo sapiens protein kinase homolog (BUBR1) mRNA; complete cds |
| 3 | RC_AA252672_s | diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2 |
| 3 | RC_AA256157 | ESTs |
| 4 | RC_AA256680 | ESTs |
| 3 | RC_AA258873 | ESTs |
| 1 | RC_AA262727 | ESTs |
| 4 | RC_AA281451 | ESTs |
| 4 | RC_AA281545 | ESTs |
| 3 | RC_AA282069 | Homo sapiens mRNA for KIAA63 protein; complete cds |
| 1 | RC_AA283044 | ESTs |
| 3 | RC_AA283930 | ESTs |
| 4 | RC_AA284755 | ESTs; Weakly similar to unknown [H.sapiens] |
| 4 | RC_AA291268 | ESTs |
| 1 | RC_AA291927 | ESTs |
| 2 | RC_AA343514 | ESTs |
| 3 | RC_AA398109 | ESTs |
| 4 | RC_AA405737 | ESTs |
| 4 | RC_AA406610 | ESTs |
| 4 | RC_AA411465 | ESTs |
| 3 | RC_AA416886 | ESTs; Weakly similar to predicted using Genefinder [C.elegans] |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 4 | RC_AA424013 | Homo sapiens clone 23767 and 23782 mRNA sequences |
| 4 | RC_AA424148 | ESTs |
| 2 | RC_AA424558 | ESTs; Weakly similar to 33-kDa phototransducing protein [H.sapiens] |
| 4 | RC_AA424961_s | Homo sapiens TEB4 protein mRNA; complete cds |
| 3 | RC_AA425367 | ESTs |
| 1 | RC_AA425921 | Homo sapiens I-1 receptor candidate protein mRNA; complete cds |
| 4 | RC_AA426220 | Homo sapiens mRNA for KIAA523 protein; partial cds |
| 4 | RC_AA427735 | ESTs |
| 4 | RC_AA430673 | ESTs |
| 4 | RC_AA432248 | ESTs |
| 4 | RC_AA435896 | ESTs |
| 3 | RC_AA436705 | Homo sapiens mRNA for KIAA766 protein; complete cds |
| 3 | RC_AA446561 | Homo sapiens mRNA for KIAA47 protein; complete cds |
| 4 | RC_AA448238 | Homo sapiens mRNA for KIAA915 protein; complete cds |
| 3 | RC_AA448688 | ESTs; Weakly similar to KIAA638 protein [H.sapiens] |
| 3 | RC_AA449756 | ESTs; Weakly similar to rA8 [R.norvegicus] |
| 4 | RC_AA450303 | ESTs |
| 3 | RC_AA452411 | ESTs |
| 4 | RC_AA454566 | ribosomal protein L13 |
| 4 | RC_AA454667 | ESTs |
| 4 | RC_AA456437 | ESTs |
| 4 | RC_AA456646 | ESTs |
| 4 | RC_AA456826 | ESTs |
| 4 | RC_AA456981 | ESTs |
| 4 | RC_AA458959 | ESTs |
| 3 | RC_AA459950 | ESTs |
| 3 | RC_AA460449 | ESTs; Highly similar to PROBABLE PHOSPHOSERINE AMINOTRANSFERASE [Oryctolagus cuniculus] |
| 3 | RC_AA463910 | ESTs |
| 4 | RC_AA464603 | ESTs |
| 3 | RC_AA464606 | ESTs |
| 4 | RC_AA465093 | TIA1 cytotoxic granule-associated RNA-binding protein |
| 3 | RC_AA465692 | Homo sapiens mRNA for KIAA648 protein; partial cds |
| 3 | RC_AA476473 | Homo sapiens Trio mRNA; complete cds |
| 1 | RC_AA478109 | ESTs |
| 4 | RC_AA478474 | ESTs |
| 3 | RC_AA480889 | ESTs |
| 1 | RC_AA485223 | ESTs |
| 1 | RC_AA485254 | ESTs |
| 4 | RC_AA486183 | ESTs; Weakly similar to Yhr1wp [S.cerevisiae] |
| 3 | RC_AA496936 | ESTs; Weakly similar to B cell growth factor [H.sapiens] |
| 4 | RC_AA598589 | ESTs |
| 4 | RC_AA598831_f | ESTs |
| 4 | RC_AA600150 | ESTs |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 4 | RC_AA608545 | ESTs |
| 3 | RC_AA609210 | ESTs |
| 3 | RC_AA610108 | ESTs; Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.5C [Schizosaccharomyces pombe] |
| 4 | RC_AA620582 | ESTs; Weakly similar to (defline not available 424227) [H.sapiens] |
| 4 | RC_AA621239 | ESTs; Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R1E12.1 IN CHROMOSOME III [Caenorhabditis elegans] |
| 3 | RC_AA621714 | ESTs |
| 1 | RC_AA621718 | ESTs |
| 1 | RC_D19673 | ESTs |
| 1 | RC_D25755_s | ESTs |
| 1 | RC_D51095 | ESTs |
| 4 | RC_D60272_I | ESTs; Weakly similar to macrophage lectin 2 [H.sapiens] |
| 2 | T08879 | cathepsin F |
| 3 | T34527 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) |
| 2 | T40327_s | ESTs |
| 3 | T62771_s | Homo sapiens nucleoplasmin-3 (NPM3) mRNA; complete cds |
| 1 | T63174_s | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] |
| 2 | T83444 | Homo sapiens mRNA for KIAA887 protein; partial cds |
| 1 | T93641 | ESTs |
| 2 | U48263 | prepronociceptin |
| 2 | U49065 | interleukin 1 receptor-like 2 |
| 2 | U79300 | Human clone 23629 mRNA sequence |
| 1 | U88573 | Human NBR2 mRNA; complete cds |
| 2 | U93867 | Human RNA polymerase III subunit (RPC62) mRNA; complete cds |
| 4 | W01094 | ESTs |
| 2 | W01568 | ESTs |
| 2 | W26853 | ESTs |
| 2 | W27179 | BCL2/adenovirus E1B 19kD-interacting protein 3-like |
| 2 | W27965 | epimorphin |
| 3 | W36280_s | Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA; complete cds |
| 2 | W47063 | ESTs |
| 4 | W79060 | ESTs; Weakly similar to Ras-binding protein SUR-8 [M.musculus] |
| 4 | W88550 | ESTs; Moderately similar to trg gene product [R.norvegicus] |
| 1 | X60486 | H4 histone family; member G |
| 2 | X78931_s | H.sapiens HZF8 mRNA for zinc finger protein |
| 1 | Z14077_s | YY1 transcription factor |
| 1 | RC_AA002147 | EST |
| 1 | RC_AA004711 | ESTs |
| 1 | RC_AA010383 | EST |
| 1 | RC_AA015761 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 2 | RC_AA018772 | ESTs |
| 2 | RC_AA021473_r | EST |
| 2 | RC_AA024835 | potassium voltage-gated channel; delayed-rectifier; subfamily S; member 3 |
| 2 | RC_AA025858 | ESTs |
| 1 | RC_AA027229 | ESTs |
| 1 | RC_AA029428 | ESTs |
| 3 | RC_AA035143 | ESTs |
| 1 | RC_AA035237 | ESTs |
| 2 | RC_AA039347 | EST |
| 1 | RC_AA040740 | ESTs |
| 3 | RC_AA041551 | ESTs |
| 1 | RC_AA045513 | ESTs |
| 1 | RC_AA045745 | EST |
| 1 | RC_AA055348 | ESTs |
| 2 | RC_AA056582_s | ESTs |
| 1 | RC_AA056697 | ESTs |
| 1 | RC_AA056746 | EST |
| 3 | RC_AA057678 | ESTs |
| 2 | RC_AA058681 | ESTs |
| 2 | RC_AA058686 | ESTs |
| 2 | RC_AA062840 | zm5c1.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE:513234 3' similar to gb:S71381 PROTEASOME BETA CHAIN (HUMAN);, mRNA sequence |
| 2 | RC_AA064859 | zm5f3.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone IMAGE:52985 3', mRNA sequence |
| 1 | RC_AA065069 | zm12e11.s1 Stratagene pancreas (#93728) Homo sapiens cDNA clone IMAGE:525452 3', mRNA sequence |
| 1 | RC_AA069923 | zm67g3.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:5374 3' similar to gb:S66915_cds1 ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence |
| 2 | RC_AA070799_s | zm6h5.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone IMAGE:5373 3', mRNA sequence |
| 2 | RC_AA070815 | zm6a1.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone IMAGE:529992 3' similar to gb:X67951 PROLIFERATION-ASSOCIATED PROTEIN PAG (HUMAN);, mRNA sequence |
| 2 | RC_AA075374 | zm87a1.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:544872 3', mRNA sequence |
| 2 | RC_AA076382 | zm91g8.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545342 3', mRNA sequence |
| 1 | RC_AA078787 | ESTs |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 2 | RC_AA078986 | zm92h1.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545425 3', mRNA sequence |
| 1 | RC_AA079393 | zm95h11.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:545733 3' similar to gb:X1656 CYTOCHROME C OXIDASE POLYPEPTIDE VIIC PRECURSOR (HUMAN);, mRNA sequence |
| 2 | RC_AA079487 | zm97f8.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:545895 3', mRNA sequence |
| 2 | RC_AA083207 | EST |
| 2 | RC_AA083256 | vinculin |
| 2 | RC_AA084415 | zn6g9.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546688 3', mRNA sequence |
| 2 | RC_AA085274 | zn1f1.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:546169 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);, mRNA sequence |
| 2 | RC_AA088678 | ESTs |
| 3 | RC_AA100925 | ESTs; Weakly similar to predicted using Genefinder [C.elegans] |
| 3 | RC_AA101255 | ESTs; Highly similar to J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN [Homo sapiens] |
| 3 | RC_AA126474 | stanniocalcin 2 |
| 2 | RC_AA127017 | ESTs |
| 2 | RC_AA129968 | ESTs; Weakly similar to protein phosphatase 2A 13 kDa regulatory subunit [H.sapiens] |
| 2 | RC_AA130240 | ESTs |
| 1 | RC_AA131866 | ESTs |
| 2 | RC_AA132039 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_AA132983 | ESTs; Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE; CYTOPLASMIC [Saccharomyces cerevisiae] |
| 3 | RC_AA133250 | ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans] |
| 1 | RC_AA133583_s | high-mobility group (nonhistone chromosomal) protein isoform I-C |
| 4 | RC_AA135941 | ESTs |
| 2 | RC_AA148650 | zo9e6.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:56722 3', mRNA sequence |
| 2 | RC_AA151110 | ESTs |
| 2 | RC_AA155754 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] |
| 4 | RC_AA156125 | ESTs |
| 2 | RC_AA156289 | ESTs |
| 1 | RC_AA156997 | ESTs |
| 2 | RC_AA157291 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 2 | RC_AA157293 | ESTs |
| 2 | RC_AA164293_f | ESTs |
| 1 | RC_AA164676 | EST |
| 1 | RC_AA167375 | Homo sapiens mRNA for KIAA53 protein; partial cds |
| 1 | RC_AA167550 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] |
| 2 | RC_AA176589 | EST |
| 1 | RC_AA180448 | EST |
| 4 | RC_AA187144_s | endothelin 1 |
| 3 | RC_AA189170_f | ESTs |
| 4 | RC_AA192757 | ESTs |
| 2 | RC_AA205650 | ESTs |
| 4 | RC_AA233342 | ESTs; Weakly similar to neural differentiation-associated protein [M.musculus] |
| 3 | RC_AA233472 | ESTs |
| 2 | RC_AA234110 | ESTs |
| 4 | RC_D80981 | ESTs |
| 3 | RC_F01660 | ESTs; Weakly similar to HYPOTHETICAL PROTEIN HI34 [Haemophilus influenzae] |
| 1 | RC_F02206 | EST; Highly similar to ether-a-go-go-related protein [H.sapiens] |
| 4 | RC_F02208 | ESTs |
| 4 | RC_F02544 | ESTs |
| 4 | RC_F03918 | ESTs |
| 4 | RC_F04258_s | ESTs; Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus] |
| 4 | RC_F04600 | ESTs |
| 4 | RC_F08998 | ESTs |
| 2 | RC_F09605 | ESTs |
| 4 | RC_F11115 | ESTs |
| 3 | RC_H06371 | ESTs |
| 1 | RC_H10995 | ESTs |
| 1 | RC_H11938 | ESTs; Weakly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae] |
| 4 | RC_H16568 | ESTs |
| 4 | RC_H16772 | ESTs |
| 1 | RC_H18951 | ESTs; Moderately similar to seven-pass transmembrane receptor precursor [M.musculus] |
| 1 | RC_H20859 | ESTs |
| 1 | RC_H23747 | ESTs |
| 1 | RC_H38087 | ESTs |
| 1 | RC_H40331 | ESTs |
| 1 | RC_H40567 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 1 | RC_H46966 | ESTs |
| 1 | RC_H56640_l | yq99a5.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:23888 3', mRNA sequence |
| 1 | RC_H57154 | ESTs; Weakly similar to RST [M.musculus] |
| 1 | RC_H96712 | ESTs |
| 1 | RC_N20814 | ESTs |
| 3 | RC_N25249 | synaptosomal-associated protein; 23kD |
| 1 | RC_N27100 | ESTs |
| 1 | RC_N39616 | RNA (guanine-7-) methyltransferase |
| 1 | RC_N48982 | ESTs |
| 1 | RC_N51957 | ESTs |
| 1 | RC_N52271 | Homo sapiens LIM protein mRNA; complete cds |
| 1 | RC_N59435 | ESTs; Weakly similar to No definition line found [H.sapiens] |
| 1 | RC_N64139 | ESTs; Weakly similar to Ndr protein kinase [H.sapiens] |
| 3 | RC_N66981 | ESTs |
| 1 | RC_N68640 | ESTs |
| 4 | RC_N69352 | ESTs; Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae] |
| 4 | RC_N95226 | Homo sapiens mRNA for KIAA758 protein; partial cds |
| 1 | RC_R00138 | ESTs |
| 1 | RC_R07998 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 1 | RC_R08929 | ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7) |
| 1 | RC_R10307 | ESTs |
| 3 | RC_R33354 | ESTs |
| 1 | RC_R36083 | ESTs |
| 1 | RC_R37938_f | ESTs |
| 1 | RC_R39330 | yd1g4.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24282 3', mRNA sequence |
| 1 | RC_R40816_s | cullin 4A |
| 1 | RC_R43162_s | ESTs |
| 3 | RC_R45698 | ESTs; Weakly similar to Similarity to Salmonella regulatory protein UHPC [C.elegans] |
| 2 | RC_R54554 | ESTs |
| 1 | RC_R68425 | ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens] |
| 1 | RC_R68568 | ESTs |
| 3 | RC_R68763 | ESTs |
| 1 | RC_R70467 | ESTs |
| 1 | RC_R73565 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] |
| 4 | RC_R73640 | ESTs |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 1 | RC_R78376 | EST |
| 1 | RC_R92453 | EST |
| 1 | RC_T03865 | ESTs |
| 3 | RC_T03872 | ESTs |
| 1 | RC_T10072 | ESTs |
| 1 | RC_T10080 | ESTs |
| 1 | RC_T10132 | Homo sapiens mRNA for KIAA478 protein; complete cds |
| 1 | RC_T15343 | ESTs |
| 2 | RC_T23457 | ESTs |
| 1 | RC_T23555 | ESTs |
| 2 | RC_T23670 | ESTs |
| 4 | RC_T23948 | ESTs |
| 4 | RC_T33464 | ESTs |
| 1 | RC_T34413 | ESTs |
| 2 | RC_T34611 | ESTs |
| 2 | RC_T40920 | ESTs |
| 4 | RC_T55182 | ESTs |
| 2 | RC_T77453 | EST |
| 1 | RC_T84039 | ESTs |
| 1 | RC_T86458 | ESTs |
| 1 | RC_T87693 | ESTs |
| 2 | RC_T89350_s | ESTs |
| 1 | RC_T90945 | ESTs |
| 2 | RC_T90987 | ESTs |
| 1 | RC_T91863 | ESTs |
| 1 | RC_T91881 | EST |
| 1 | RC_T93783_s | ESTs |
| 1 | RC_T96687 | ESTs |
| 2 | RC_T96944 | ESTs |
| 3 | RC_T97307 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] |
| 1 | RC_T97764 | ESTs |
| 2 | RC_W48817 | ESTs |
| 2 | RC_W58343 | ESTs |
| 1 | RC_W59949 | ESTs; Highly similar to RAS-LIKE PROTEIN TC1 [Homo sapiens] |
| 1 | RC_W74644 | ESTs |
| 1 | RC_W74761 | ESTs; Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis elegans] |
| 1 | RC_W74802 | ESTs |
| 1 | RC_W81205 | ESTs |
| 2 | RC_W81237 | ESTs |
| 3 | RC_W90146_f | ESTs |
| 1 | RC_W92798 | ESTs |
| 1 | RC_Z38412 | EST |
| 1 | RC_Z38709 | inositol 1;4;5-triphosphate receptor; type 2 |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 1 | RC_Z38904 | ESTs |
| 2 | RC_Z39103 | core-binding factor; runt domain; alpha subunit 2; translocated to; 2 |
| 2 | RC_Z39930_f | ESTs |
| 2 | RC_Z39939 | ESTs |
| 3 | RC_Z40012_i | Homo sapiens mRNA for KIAA587 protein; complete cds |
| 2 | RC_Z40377_s | ESTs |
| 1 | RC_Z40820 | ESTs |
| 3 | RC_Z41680 | ESTs |
| 4 | AFFX-BioB-3 | . |
| 2 | RC_AA005112 | Human zinc-finger domain-containing protein mRNA; partial cds |
| 4 | RC_AA005432 | ESTs; Highly similar to ANTI-SILENCING PROTEIN 1 [Saccharomyces cerevisiae] |
| 4 | RC_AA010163 | Human mRNA for KIAA312 gene; partial cds |
| 4 | RC_AA026356 | ESTs |
| 2 | RC_AA026901 | ESTs |
| 4 | RC_AA036867 | ESTs |
| 1 | RC_AA044644 | Pp52 |
| 4 | RC_AA046426 | Homo sapiens MSE55-related protein (UB1) mRNA; complete cds |
| 4 | RC_AA054515 | ESTs; Weakly similar to X-linked retinopathy protein {C-terminal; clone XEH.8c} [H.sapiens] |
| 2 | RC_AA084162 | zn17h6.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:547739 3', mRNA sequence |
| 4 | RC_AA085749 | Homo sapiens mRNA for ATP binding protein; complete cds |
| 4 | RC_AA098874 | ESTs |
| 2 | RC_AA101056 | zn25b3.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548429 3' similar to contains L1.b3 L1 repetitive element ;, mRNA sequence |
| 1 | RC_AA102746 | ESTs; Moderately similar to cytotoxic ligand TRAIL receptor [H.sapiens] |
| 2 | RC_AA114250_s | Homo sapiens mRNA for KIAA512 protein; complete cds |
| 4 | RC_AA126561_s | ESTs |
| 4 | RC_AA128980_i | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 4 | RC_AA129757 | ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L22 [Rattus norvegicus] |
| 4 | RC_AA129921 | ESTs |
| 2 | RC_AA133331 | Homo sapiens mRNA for KIAA741 protein; complete cds |
| 2 | RC_AA135958 | ESTs |
| 4 | RC_AA136524_s | ESTs |
| 4 | RC_AA147044 | ESTs; Weakly similar to transformation-related protein [H.sapiens] |
| 4 | RC_AA148885 | ESTs |
| 4 | RC_AA150043 | ESTs |
| 2 | RC_AA151621 | ESTs |
| 4 | RC_AA155743 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 2 | RC_AA156335 | ESTs |
| 4 | RC_AA156336 | Homo sapiens nuclear receptor co-repressor N-CoR mRNA; complete cds |
| 2 | RC_AA159181 | ESTs |
| 2 | RC_AA159825 | ESTs |
| 2 | RC_AA234185 | ESTs |
| 4 | RC_AA234929 | ESTs |
| 1 | RC_AA234935 | ESTs |
| 4 | RC_AA236359 | ESTs |
| 2 | RC_AA236466 | ESTs |
| 2 | RC_AA236535 | ESTs |
| 4 | RC_AA236935_s | Human normal keratinocyte mRNA |
| 2 | RC_AA236942 | ESTs |
| 4 | RC_AA237018 | ESTs |
| 2 | RC_AA237025 | ESTs |
| 2 | RC_AA242751 | Homo sapiens mRNA for KIAA93 protein; partial cds |
| 3 | RC_AA242760 | ESTs |
| 3 | RC_AA242763 | Homo sapiens Cdc14B1 phosphatase mRNA; complete cds |
| 2 | RC_AA242809 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_AA243133 | ESTs; Highly similar to SERINE/THREONINE-PROTEIN KINASE IPL1 [Saccharomyces cerevisiae] |
| 4 | RC_AA243495 | ESTs |
| 3 | RC_AA243706 | ESTs |
| 4 | RC_AA250848 | zs6e2.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:68441 3', mRNA sequence |
| 2 | RC_AA250868 | ESTs |
| 4 | RC_AA251152 | ESTs |
| 2 | RC_AA251544_s | ESTs |
| 4 | RC_AA251792 | ESTs |
| 4 | RC_AA252063 | Homo sapiens mRNA for PCDH7 (BH-Pcdh)c; complete cds |
| 3 | RC_AA252144 | ESTs |
| 4 | RC_AA252524 | ESTs |
| 3 | RC_AA253461 | ESTs |
| 4 | RC_AA255522 | ESTs |
| 2 | RC_AA256468 | ESTs |
| 4 | RC_AA256528 | ESTs |
| 2 | RC_AA257976 | ESTs |
| 4 | RC_AA258296 | Homo sapiens mRNA for KIAA579 protein; partial cds |
| 3 | RC_AA258409 | H.sapiens gene from PAC 313L4; similar to Myelin PO |
| 2 | RC_AA258421 | Homo sapiens clone 683 unknown mRNA; complete sequence |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 3 | RC_AA262077 | Human NAD+-dependent succinate-semialdehyde dehydrogenase (SSADH) mRNA; 3' end |
| 4 | RC_AA278650 | ESTs |
| 2 | RC_AA278766 | ESTs |
| 4 | RC_AA279667_s | natural killer-tumor recognition sequence |
| 3 | RC_AA280791 | eukaryotic translation initiation factor 5 |
| 4 | RC_AA280819 | ESTs |
| 4 | RC_AA280828 | ESTs |
| 4 | RC_AA282195 | ESTs; Weakly similar to ORF YNL292w [S.cerevisiae] |
| 2 | RC_AA283127_s | Homo sapiens clone LM1955 H15e3 gene; partial cds |
| 2 | RC_AA284694 | Homo sapiens CG1 mRNA; complete cds |
| 3 | RC_AA291137 | ESTs |
| 3 | RC_AA291708 | ESTs; Moderately similar to hypothetical protein [H.sapiens] |
| 3 | RC_AA293495 | Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene; complete sequence |
| 4 | RC_AA347193 | ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans] |
| 4 | RC_AA398474_s | ESTs |
| 4 | RC_AA398512 | ESTs |
| 2 | RC_AA400277 | ESTs; Weakly similar to putative p15 [H.sapiens] |
| 4 | RC_AA400896 | ESTs |
| 3 | RC_AA404494 | CTP synthase |
| 2 | RC_AA410345 | ESTs; Weakly similar to A33 antigen precursor [H.sapiens] |
| 4 | RC_AA416733 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] |
| 4 | RC_AA425154 | ESTs |
| 4 | RC_AA426573 | ESTs |
| 2 | RC_AA431418 | N-acetylglucosaminidase; alpha- (Sanfilippo disease IIIB) |
| 4 | RC_AA436182 | ESTs |
| 2 | RC_AA437099 | ESTs |
| 4 | RC_AA446585 | ESTs |
| 3 | RC_AA446887 | ESTs |
| 2 | RC_AA447224 | ESTs; Highly similar to HYPOTHETICAL 8.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae] |
| 2 | RC_AA447709 | ESTs; Moderately similar to putative transcription factor CA15 [H.sapiens] |
| 4 | RC_AA453624 | deoxynucleotidyltransferase; terminal |
| 4 | RC_AA455044 | ESTs |
| 4 | RC_AA456045 | ESTs |
| 4 | RC_AA460454_s | ESTs; Weakly similar to KIAA512 protein [H.sapiens] |
| 4 | RC_AA476494 | ESTs; Weakly similar to KIAA512 protein [H.sapiens] |
| 4 | RC_AA476738 | ESTs; Highly similar to FLI-LRR associated protein-1 [M.musculus] |
| 4 | RC_AA481422 | Homo sapiens mRNA for H-2K binding factor-2; complete cds |
| 3 | RC_AA482269 | Integral membrane protein 1 |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 2 | RC_AA482595 | ESTs; Highly similar to p36 |
| 4 | RC_AA485084_s | ESTs |
| 4 | RC_AA485431_s | ESTs |
| 4 | RC_AA489057 | H.sapiens mRNA for nuclear protein SA-2 |
| 4 | RC_AA489638 | ESTs |
| 2 | RC_AA491000 | ESTs |
| 3 | RC_AA491250 | ESTs |
| 4 | RC_AA505133 | ESTs |
| 4 | RC_AA598447 | Homo sapiens exportin t mRNA; complete cds |
| 3 | RC_AA599243 | ESTs |
| 3 | RC_AA599574_i | ESTs |
| 4 | RC_AA600153 | DEK gene |
| 4 | RC_AA609309 | ESTs |
| 4 | RC_AA609710 | ESTs; Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI4-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae] |
| 4 | RC_AA610068 | H.sapiens mRNA for PIBF1 protein; complete |
| 1 | RC_AA621399 | ESTs |
| 4 | RC_AA621752 | Human 26S proteasome-associated pad1 homolog (POH1) mRNA; complete cds |
| 2 | RC_C21523 | ESTs |
| 2 | RC_D12160 | ESTs; Weakly similar to unknown [H.sapiens] |
| 4 | RC_D19708 | ESTs |
| 2 | RC_D25801 | ESTs; Highly similar to KIAA445 protein [H.sapiens] |
| 2 | RC_D45652 | ESTs; Weakly similar to unknown [H.sapiens] |
| 4 | RC_D60208_f | ESTs |
| 3 | RC_D80504_s | zinc finger protein 198 |
| 2 | RC_F03010 | ESTs; Weakly similar to ZINC FINGER PROTEIN HRX [Homo sapiens] |
| 4 | RC_F04247 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens] |
| 4 | RC_F10966 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 4 | RC_F13700 | Homo sapiens ribonuclease P protein subunit p4 (RPP4) gene; complete cds |
| 4 | RC_H05063 | ESTs |
| 4 | RC_H16758 | ESTs; Highly similar to ERYTHROPOIETIN RECEPTOR PRECURSOR [Homo sapiens] |
| 4 | RC_H17315_s | karyopherin alpha 1 (importin alpha 5) |
| 4 | RC_H22556 | PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG |
| 4 | RC_H22566 | ESTs; Highly similar to protein tyrosine phosphatase epsilon cytoplasmic isoform [H.sapiens] |
| 4 | RC_H48459_s | Human mRNA for KIAA186 gene; complete cds |
| 4 | RC_H53073 | ESTs |
| 2 | RC_H56559_s | Homo sapiens mRNA for KIAA61 protein; partial cds |
| 3 | RC_H57957_s | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 2 | RC_H64938_s | ESTs |
| 2 | RC_H64973 | ESTs |
| 4 | RC_H69535 | ESTs |
| 2 | RC_H73110 | ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens] |
| 2 | RC_H81783 | ESTs |
| 1 | RC_H86259 | Homo sapiens chromosome 19; cosmid R32611 |
| 2 | RC_H88353 | ESTs; Weakly similar to reverse transcriptase related protein [H.sapiens] |
| 2 | RC_H88639 | ESTs |
| 4 | RC_H88675 | ESTs |
| 4 | RC_H93708_s | CLEAVAGE SIGNAL-1 PROTEIN |
| 4 | RC_N22107 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_N24046 | ESTs; Weakly similar to 6S RIBOSOMAL PROTEIN L1 [Homo sapiens] |
| 2 | RC_N27028 | ESTs |
| 2 | RC_N30205 | ESTs; Weakly similar to hypothetical protein [H.sapiens] |
| 1 | RC_N30621 | ESTs |
| 4 | RC_N33258 | Homo sapiens nuclear receptor co-repressor N-CoR mRNA; complete cds |
| 2 | RC_N33390 | EST |
| 2 | RC_N40180 | EST; Weakly similar to putative p15 [H.sapiens] |
| 2 | RC_N45198 | EST |
| 3 | RC_N45979_s | SH3 domain protein 1B |
| 2 | RC_N48325 | EST |
| 2 | RC_N48913 | ESTs |
| 4 | RC_N49394 | Homo sapiens mRNA for KIAA716 protein; complete cds |
| 1 | RC_N50656 | ESTs; Highly similar to mosaic protein LR11 [H.sapiens] |
| 4 | RC_N50721 | kinesin family protein 3B |
| 4 | RC_N53143 | ESTs |
| 2 | RC_N53359 | ESTs |
| 4 | RC_N55326 | ESTs |
| 2 | RC_N55493 | yv5c2.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246146 3', mRNA sequence |
| 4 | RC_N57493 | EST |
| 2 | RC_N62955 | ESTs; Weakly similar to ankyrin G [H.sapiens] |
| 4 | RC_N63520 | EST; Weakly similar to mariner transposase [H.sapiens] |
| 4 | RC_N63604 | ESTs |
| 2 | RC_N64166 | frizzled (Drosophila) homolog 7 |
| 2 | RC_N64168 | ESTs |
| 2 | RC_N64191 | ESTs |
| 4 | RC_N66845 | ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens] |
| 4 | RC_N67135 | ESTs |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 2 | RC_N67295 | ESTs |
| 4 | RC_N68399 | H2B histone family; member N |
| 4 | RC_N68963 | ESTs |
| 4 | RC_N69331 | peptidylprolyl isomerase C (cyclophilin C) |
| 2 | RC_N70777 | ESTs |
| 1 | RC_N71364_s | ESTs; Weakly similar to transformation-related protein [H.sapiens] |
| 4 | RC_N71545_s | ESTs; Moderately similar to hypothetical protein [H.sapiens] |
| 2 | RC_N71571 | ESTs |
| 4 | RC_N74456 | EST |
| 4 | RC_N75594 | ESTs |
| 2 | RC_N79035 | EST |
| 2 | RC_N80279 | ESTs; Highly similar to (defline not available 4239677) [H.sapiens] |
| 4 | RC_N91797 | ESTs |
| 4 | RC_N92454 | karyopherin (importin) beta 1 |
| 4 | RC_N94581 | actin; beta |
| 4 | RC_N94746 | ESTs |
| 4 | RC_N98238 | ESTs |
| 4 | RC_R02384 | EST |
| 2 | RC_R16833 | ESTs; Weakly similar to !!!! ALU CLASS F WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_R41828_s | myosin VA (heavy polypeptide 12; myoxin) |
| 2 | RC_R43203 | ESTs |
| 4 | RC_R46395 | ESTs; Moderately similar to Unknown gene product [H.sapiens] |
| 2 | RC_R58863 | ESTs |
| 2 | RC_R78248 | ESTs |
| 4 | RC_T11483 | ESTs |
| 4 | RC_T16896 | ESTs |
| 2 | RC_T23820 | cyclin T2 |
| 4 | RC_T30222 | ESTs; Weakly similar to tetracycline transporter-like protein [M.musculus] |
| 4 | RC_W15275_s | ESTs |
| 2 | RC_W38194 | Accession not listed in Genbank |
| 3 | RC_W42414_s | ESTs |
| 4 | RC_W46577_s | H.sapiens mRNA for ESM-1 protein |
| 4 | RC_W49632_s | Human clone 2398 mRNA sequence |
| 2 | RC_W57613 | ESTs |
| 2 | RC_W57759 | EST |
| 4 | RC_W61118 | ESTs |
| 4 | RC_W65344 | ESTs; Highly similar to ICH-2 PROTEASE PRECURSOR [Homo sapiens] |
| 2 | RC_W69216 | ESTs |
| 2 | RC_W69379 | ESTs; Weakly similar to mitochondrial inner membrane protease 1 [S.cerevisiae] |
| 4 | RC_W86728 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 4 | RC_Z38499 | ESTs; Weakly similar to protein phosphatase [H.sapiens] |
| 2 | RC_Z38630 | Homo sapiens 1kD protein (BC1) mRNA; complete cds |
| 4 | RC_Z39494 | ESTs |
| 4 | RC_Z39623 | ESTs |
| 3 | RC_Z40071_s | BMX non-receptor tyrosine kinase |
| 2 | RC_Z40174 | EST |
| 2 | RC_Z40182 | EST |
| 2 | RC_Z40904 | EST |
| 4 | AFFX-BioB-3 | . |
| 4 | AFFX-BioC-3 | . |
| 3 | AFFX-DapX-5 | . |
| 1 | AFFX-LysX-M | . |
| 3 | RC_AA166965 | ESTs |
| 3 | RC_AA167500 | EST |
| 1 | RC_AA169599_s | ESTs |
| 3 | RC_AA171724 | ESTs |
| 2 | RC_AA171739 | ESTs |
| 3 | RC_AA177105 | ESTs |
| 2 | RC_AA182626 | ESTs |
| 3 | RC_AA186324 | ESTs; Highly similar to cell cycle progression restoration 8 protein [H.sapiens] |
| 1 | RC_AA192099 | zinc finger protein 148 (pHZ-52) |
| 3 | RC_AA192173 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_AA192415 | EST |
| 3 | RC_AA192553 | ESTs; Moderately similar to RGC-32 [R.norvegicus] |
| 3 | RC_AA194851 | ESTs |
| 3 | RC_AA195520_s | ESTs |
| 3 | RC_AA196300 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_AA196517 | Lon protease-like protein |
| 3 | RC_AA196549 | ESTs |
| 3 | RC_AA196721 | zq9a3.s1 Stratagene muscle 93729 Homo sapiens cDNA clone IMAGE:629164 3' similar to TR:G746415 G746415 I KAPPA BR. ;, mRNA sequence |
| 3 | RC_AA196729_i | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 1 | RC_AA196979 | ESTs; Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens] |
| 2 | RC_AA206828 | ESTs; Weakly similar to ubiquitous TPR motif; Y isoform [H.sapiens] |
| 3 | RC_AA207123 | immunoglobulin superfamily; member 3 |
| 1 | RC_AA214539_i | ESTs |
| 3 | RC_AA226914_s | TR2 nuclear hormone receptor |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 3 | RC_AA227260 | Zic family member 3 (odd-paired Drosophila homolog; heterotaxy 1) |
| 3 | RC_AA227469 | EST |
| 3 | RC_AA233122 | ESTs; Highly similar to CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN [Rattus norvegicus] |
| 3 | RC_AA233334_s | Homo sapiens josephin MJD1 mRNA; cds |
| 3 | RC_AA233347 | Homo sapiens zinc finger protein 216 splice variant 2 (ZNF216) mRNA; complete cds |
| 1 | RC_AA233519 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] |
| 1 | RC_AA233714 | Apg12 (autophagy; yeast) homolog |
| 1 | RC_AA233796 | ESTs |
| 1 | RC_AA235050_f | ESTs |
| 1 | RC_AA235704 | ESTs; Weakly similar to Wiscott-Aldrich Syndrome protein homolog [M.musculus] |
| 3 | RC_AA236031 | ESTs |
| 1 | RC_AA236352 | ESTs |
| 1 | RC_AA236390_s | ESTs |
| 1 | RC_AA236453 | ESTs |
| 3 | RC_AA243370 | EST |
| 2 | RC_AA250947 | ESTs |
| 3 | RC_AA251083 | ESTs |
| 3 | RC_AA251113 | ESTs |
| 4 | RC_AA251973 | ESTs |
| 3 | RC_AA252023 | ESTs; Moderately similar to (defline not available 397874) [H.sapiens] |
| 1 | RC_AA252414 | ESTs |
| 1 | RC_AA252650 | protein kinase; mitogen-activated; kinase 7 (MAP kinase kinase 7) |
| 3 | RC_AA255523 | ESTs |
| 3 | RC_AA258128 | ESTs |
| 3 | RC_AA262105 | Human mRNA for KIAA331 gene; complete cds |
| 1 | RC_AA262107 | ESTs |
| 1 | RC_AA262235 | ESTs |
| 3 | RC_AA278298 | zs8b3.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:73757 3', mRNA sequence |
| 1 | RC_AA278529_i | ESTs; Highly similar to serine/threonine protein kinase [H.sapiens] |
| 1 | RC_AA278721 | ESTs |
| 1 | RC_AA280036 | ESTs |
| 1 | RC_AA280648 | ESTs; Weakly similar to rab-related GTP-binding protein [H.sapiens] |
| 1 | RC_AA280738 | ESTs |
| 3 | RC_AA280794 | ESTs |
| 1 | RC_AA280837 | ESTs |
| 1 | RC_AA280886 | ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens] |
| 1 | RC_AA280934 | ESTs |
| 1 | RC_AA281535 | Homo sapiens mRNA for KIAA879 protein; complete cds |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 4 | RC_AA281797_s | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds |
| 1 | RC_AA282047 | ESTs |
| 1 | RC_AA283002 | Human zinc finger protein (SRE-ZBP) mRNA; 3' end |
| 3 | RC_AA283709 | ESTs |
| 1 | RC_AA283902 | ESTs; Weakly similar to X-linked retinopathy protein {C-terminal; clone XEH.8c} [H.sapiens] |
| 1 | RC_AA284108 | Human DNA from chromosome 19-specific cosmid F25965; genomic sequence |
| 1 | RC_AA284109 | Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene; an unknown putative gene; a pseudogene with high similarity to part of antigen KI-67; a pu |
| 1 | RC_AA284371 | Homo sapiens clone 23967 unknown mRNA; partial cds |
| 3 | RC_AA284744_f | ESTs |
| 1 | RC_AA284784 | ESTs |
| 1 | RC_AA284840 | ESTs |
| 1 | RC_AA286844 | ESTs |
| 3 | RC_AA287032 | ESTs |
| 1 | RC_AA287038 | EST |
| 1 | RC_AA287546 | ESTs |
| 1 | RC_AA287553_s | ESTs |
| 3 | RC_AA287556 | ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens] |
| 1 | RC_AA287564 | ribosomal protein L37 |
| 1 | RC_AA291015_s | CDC7 (cell division cycle 7; S. cerevisiae; homolog)-like 1 |
| 3 | RC_AA291716 | EST |
| 1 | RC_AA291749_s | ESTs |
| 1 | RC_AA293656 | EST |
| 1 | RC_AA302430 | ESTs |
| 3 | RC_AA302809 | EST |
| 1 | RC_AA302820_s | purinergic receptor P2X; ligand-gated ion channel; 4 |
| 1 | RC_AA310499 | ESTs |
| 1 | RC_AA321890 | EST24442 Cerebellum II Homo sapiens cDNA 3' end, mRNA sequence |
| 1 | RC_AA340589 | EST |
| 1 | RC_AA340622 | ESTs |
| 1 | RC_AA342457_i | ESTs |
| 3 | RC_AA342828_s | glycoprotein V (platelet) |
| 1 | RC_AA342864 | ESTs |
| 1 | RC_AA342973 | ESTs |
| 1 | RC_AA346495 | ESTs |
| 1 | RC_AA347573 | Homo sapiens KIAA45 mRNA; complete cds |
| 1 | RC_AA347614 | ESTs |
| 1 | RC_AA347717 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 1 | RC_AA348913 | ESTs |
| 1 | RC_AA349647 | EST |
| 1 | RC_AA349773 | ESTs |
| 1 | RC_AA350541_s | ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens] |
| 1 | RC_AA357159_i | EST |
| 3 | RC_AA357172_i | ESTs |
| 1 | RC_AA369856_s | Human hVps41p (hVPS41) mRNA; alternative splice variant; partial cds |
| 1 | RC_AA370132 | EST |
| 1 | RC_AA370472_s | ESTs |
| 1 | RC_AA370867 | ESTs |
| 3 | RC_AA377296 | ESTs |
| 4 | RC_AA383902 | ESTs |
| 3 | RC_AA385934 | EST; Highly similar to predicted using Genefinder [C.elegans] |
| 3 | RC_AA386255 | EST |
| 1 | RC_AA386260 | EST |
| 2 | RC_AA386266 | ESTs; Highly similar to MEMBRANE GLYCOPROTEIN M6-B [Mus musculus] |
| 1 | RC_AA398014 | ESTs |
| 3 | RC_AA398222 | ESTs |
| 1 | RC_AA398235 | ESTs |
| 3 | RC_AA398348 | ESTs |
| 3 | RC_AA398482 | ESTs |
| 1 | RC_AA398504 | ESTs |
| 1 | RC_AA398505 | ESTs |
| 1 | RC_AA398507 | ESTs |
| 1 | RC_AA398523 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] |
| 1 | RC_AA398625 | ESTs |
| 4 | RC_AA398632 | ESTs |
| 3 | RC_AA398633 | ESTs |
| 3 | RC_AA398894 | ESTs |
| 3 | RC_AA398895 | EST |
| 1 | RC_AA398900 | ESTs |
| 1 | RC_AA398904 | EST |
| 1 | RC_AA399122 | ESTs; Weakly similar to mitochondrial citrate transport protein [H.sapiens] |
| 3 | RC_AA399371 | ESTs |
| 1 | RC_AA399373 | ESTs; Highly similar to KIAA568 protein [H.sapiens] |
| 1 | RC_AA399441 | ESTs |
| 3 | RC_AA399636 | ESTs |
| 1 | RC_AA399640 | ESTs |
| 1 | RC_AA399680 | ESTs |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 3 | RC_AA400080 | EST |
| 1 | RC_AA400262 | ESTs |
| 1 | RC_AA400725 | ESTs |
| 3 | RC_AA400748 | ESTs |
| 1 | RC_AA400780 | ESTs |
| 3 | RC_AA401631 | zv65b9.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758489 3', mRNA sequence |
| 1 | RC_AA401688 | ESTs |
| 1 | RC_AA401695 | EST |
| 3 | RC_AA402227 | ESTs; Moderately similar to N-tropomodulin [R.norvegicus] |
| 3 | RC_AA402329 | ESTs |
| 1 | RC_AA402398 | ESTs |
| 1 | RC_AA402449 | EST |
| 1 | RC_AA402468 | ESTs |
| 2 | RC_AA403268_s | ESTs |
| 2 | RC_AA403314 | ESTs |
| 1 | RC_AA404229 | EST |
| 1 | RC_AA404260 | ESTs |
| 1 | RC_AA404271 | Human glutamate/kainate receptor subunit (EEA3) mRNA; complete cds |
| 3 | RC_AA405026 | ESTs |
| 1 | RC_AA405182 | ESTs |
| 1 | RC_AA405237 | ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens] |
| 3 | RC_AA406061 | EST |
| 1 | RC_AA406063 | ESTs |
| 1 | RC_AA406070 | EST |
| 1 | RC_AA406137 | EST |
| 1 | RC_AA406335 | ESTs |
| 1 | RC_AA411801 | Human mRNA for KIAA37 gene; complete cds |
| 1 | RC_AA411804 | ESTs |
| 1 | RC_AA411833 | ESTs; Highly similar to (defline not available 4521278) [H.sapiens] |
| 1 | RC_AA412219 | ESTs |
| 3 | RC_AA412259 | ESTs |
| 2 | RC_AA412497 | Human Line-1 repeat mRNA with 2 open reading frames |
| 1 | RC_AA412498 | ESTs |
| 1 | RC_AA416586 | ESTs |
| 1 | RC_AA416867 | EST |
| 1 | RC_AA416874 | ESTs |
| 1 | RC_AA421133 | ESTs |
| 1 | RC_AA421138 | EST |
| 4 | RC_AA422079 | ESTs; Highly similar to ELONGATION FACTOR G; MITOCHONDRIAL PRECURSOR [Rattus norvegicus] |
| 1 | RC_AA423837 | ESTs |
| 1 | RC_AA424328 | ESTs |
| 1 | RC_AA424339 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 3 | RC_AA424469_s | ESTs |
| 1 | RC_AA424502 | ESTs |
| 3 | RC_AA425004 | ESTs |
| 1 | RC_AA425734 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] |
| 1 | RC_AA425887 | ESTs |
| 3 | RC_AA426456 | ESTs |
| 3 | RC_AA427396 | ESTs |
| 1 | RC_AA427555 | Human mRNA for KIAA23 gene; complete cds |
| 3 | RC_AA428218 | ESTs |
| 3 | RC_AA428242 | ESTs |
| 1 | RC_AA428281 | EST |
| 3 | RC_AA428865 | EST |
| 3 | RC_AA428994 | ESTs |
| 1 | RC_AA429666 | ESTs |
| 3 | RC_AA430181 | ESTs |
| 1 | RC_AA430184_s | Human putative ATP/GTP-binding protein (HEAB) mRNA; complete cds |
| 3 | RC_AA431288_s | CD3D antigen; delta polypeptide (TIT3 complex) |
| 1 | RC_AA431293 | ESTs |
| 3 | RC_AA431478 | ESTs |
| 3 | RC_AA431492 | EST |
| 1 | RC_AA431732 | EST |
| 3 | RC_AA432278 | EST |
| 4 | RC_AA434411 | ESTs |
| 3 | RC_AA435512_i | ESTs |
| 1 | RC_AA435698 | ESTs |
| 1 | RC_AA435711 | Homo sapiens mRNA for KIAA712 protein; complete cds |
| 3 | RC_AA435815_s | Clk-associating RS-cyclophilin |
| 3 | RC_AA435842 | ESTs |
| 3 | RC_AA436475 | ESTs |
| 3 | RC_AA436489 | ESTs |
| 3 | RC_AA442060 | ESTs |
| 1 | RC_AA442079 | EST |
| 3 | RC_AA443151 | ESTs |
| 4 | RC_AA446133 | ESTs |
| 1 | RC_AA447145 | Homo sapiens KIAA399 mRNA; partial cds |
| 3 | RC_AA447398 | EST |
| 1 | RC_AA447643 | ESTs |
| 1 | RC_AA447742_s | dynein; axonemal; heavy polypeptide 17-like |
| 3 | RC_AA448226 | zw96c1.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:784818 3', mRNA sequence |
| 1 | RC_AA448825 | EST |
| 1 | RC_AA449444 | ESTs |
| 3 | RC_AA450087 | regulator of Gz-selective protein signaling |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 3 | RC_AA450211 | EST |
| 1 | RC_AA450244 | ESTs |
| 3 | RC_AA452123 | ESTs; Weakly similar to Tcp-1 [M.musculus] |
| 3 | RC_AA452155 | zinc finger protein 198 |
| 3 | RC_AA452156 | EST |
| 3 | RC_AA453036 | ESTs |
| 3 | RC_AA453526 | ESTs |
| 3 | RC_AA454085 | EST |
| 3 | RC_AA454103 | ESTs |
| 1 | RC_AA454642 | ESTs |
| 1 | RC_AA454935 | ESTs |
| 3 | RC_AA456323 | ESTs |
| 3 | RC_AA457395 | EST |
| 3 | RC_AA458850 | aa26c7.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:81438 3' similar to contains L1.t3 L1 repetitive element ;, mRNA sequence |
| 3 | RC_AA459662 | EST |
| 3 | RC_AA459668 | Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA; complete cds |
| 1 | RC_AA459679_s | ESTs; Weakly similar to The KIAA191 gene is expressed ubiquitously. [H.sapiens] |
| 1 | RC_AA459702 | ESTs |
| 4 | RC_AA460017_f | ESTs |
| 3 | RC_AA460324 | ESTs |
| 3 | RC_AA461509 | ESTs; Weakly similar to hypothetical protein II [H.sapiens] |
| 3 | RC_AA464414_i | ESTs |
| 1 | RC_AA464428 | ESTs |
| 3 | RC_AA470084 | ESTs |
| 3 | RC_AA476606_s | ESTs |
| 3 | RC_AA478521 | ESTs |
| 3 | RC_AA478523 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 3 | RC_AA479949 | ESTs |
| 3 | RC_AA481252 | RAS-LIKE PROTEIN TC21 |
| 1 | RC_AA485351 | ESTs; Weakly similar to predicted using Genefinder [C.elegans] |
| 1 | RC_AA487264 | ESTs |
| 1 | RC_AA489072 | Homo sapiens mRNA for KIAA87 protein; complete cds |
| 1 | RC_AA489630 | Homo sapiens mRNA for KIAA665 protein; complete cds |
| 2 | RC_AA490225 | ESTs |
| 3 | RC_AA490227 | ESTs |
| 3 | RC_AA490255 | ESTs |
| 1 | RC_AA490890 | ESTs |
| 2 | RC_AA490916_s | ESTs |
| 3 | RC_AA490925 | Homo sapiens laforin (EPM2A) mRNA; partial cds |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 1 | RC_AA490955 | ESTs; Weakly similar to bullous pemphigoid antigen [M.musculus] |
| 1 | RC_AA495812 | ESTs |
| 3 | RC_AA495824 | ESTs |
| 1 | RC_AA496369 | ESTs |
| 3 | RC_AA504125_s | ESTs |
| 1 | RC_AA521473 | Human brain secretory protein hSec1p (HSEC1) mRNA; complete cds |
| 1 | RC_AA598440 | ESTs |
| 3 | RC_AA598899_i | ESTs |
| 3 | RC_AA599244 | Homo sapiens mRNA for KIAA53 protein; partial cds |
| 1 | RC_AA599694_s | Human mRNA for KIAA133 gene; complete cds |
| 1 | RC_AA600037 | ESTs |
| 3 | RC_AA609135 | EST |
| 1 | RC_AA609582 | Homo sapiens p6 katanin mRNA; complete cds |
| 3 | RC_AA609684 | ESTs |
| 3 | RC_AA609839 | ESTs |
| 1 | RC_AA609862 | Homo sapiens mRNA for RBP-MS/type 3; complete cds |
| 4 | RC_AA620423 | EST |
| 3 | RC_AA620747 | EST |
| 1 | RC_AA621364 | ESTs |
| 2 | RC_C20653 | ESTs |
| 3 | RC_D20085 | ESTs |
| 1 | RC_D20749 | ESTs |
| 2 | RC_D51285_s | ESTs |
| 4 | RC_D59972_i | ESTs |
| 4 | RC_F04112_f | ESTs |
| 2 | RC_F13604 | ESTs |
| 1 | RC_H01662 | ESTs |
| 1 | RC_H05135_i | ESTs |
| 3 | RC_H12245 | splicing factor; arginine/serine-rich 7 (35kD) |
| 1 | RC_H22842 | EST |
| 1 | RC_H30894 | ESTs |
| 2 | RC_H43442_s | Human mRNA for KIAA28 gene; partial cds |
| 3 | RC_H45996 | ESTs |
| 2 | RC_H69281_i | ESTs |
| 3 | RC_H69485_f | ESTs |
| 1 | RC_H69899 | ESTs; Moderately similar to unknown [H.sapiens] |
| 4 | RC_H70627_s | ESTs |
| 1 | RC_H73050_s | Rhesus blood group; D antigen |
| 1 | RC_H73260 | ESTs |
| 1 | RC_H77531_s | HIR (histone cell cycle regulation defective; S. cerevisiae) homolog A |
| 2 | RC_H80552 | EST |
| 4 | RC_H80737_s | lysyl oxidase |
| 1 | RC_H93412 | ESTs |
| 3 | RC_H94892_s | v-ral simian leukemia viral oncogene homolog A (ras related) |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 4 | RC_H95643_s | neurotrophic tyrosine kinase; receptor; type 1 |
| 2 | RC_H96552 | ESTs |
| 4 | RC_H97146 | ESTs; Highly similar to G protein-coupled receptor kinase 6; splice variant B [H.sapiens] |
| 2 | RC_H99131_s | ESTs |
| 1 | RC_H99462_s | ribosomal protein; mitochondrial; L12 |
| 1 | RC_H99837_s | ESTs |
| 2 | RC_N22140 | ESTs; Highly similar to TUBULIN GAMMA CHAIN [Euplotes octocarinatus] |
| 2 | RC_N22197 | ESTs |
| 1 | RC_N23756_s | Human mRNA for KIAA238 gene; partial cds |
| 2 | RC_N24134 | eukaryotic translation initiation factor 1A; Y chromosome |
| 4 | RC_N24195 | Homo sapiens mRNA for RanBPM; complete cds |
| 1 | RC_N26739 | CAAX box 1 |
| 2 | RC_N27098 | EST |
| 1 | RC_N27637 | ESTs |
| 4 | RC_N33090 | ESTs; Weakly similar to translation initiation factor [H.sapiens] |
| 1 | RC_N35967 | ESTs |
| 1 | RC_N38959_f | Homo sapiens chaperonin containing t-complex polypeptide 1; beta subunit (Cctb) mRNA; complete cds |
| 2 | RC_N39069 | ESTs |
| 1 | RC_N46441 | ESTs |
| 2 | RC_N48270_f | ESTs |
| 2 | RC_N48365_s | ESTs |
| 2 | RC_N51316 | ESTs |
| 1 | RC_N51499_s | ESTs |
| 4 | RC_N53976 | ESTs |
| 2 | RC_N54157 | ESTs |
| 2 | RC_N54300 | ESTs |
| 1 | RC_N54831 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] |
| 2 | RC_N59849 | ESTs |
| 4 | RC_N62132 | ESTs |
| 1 | RC_N62375 | EST |
| 4 | RC_N63138 | ESTs |
| 1 | RC_N63172 | cell division cycle 42 (GTP-binding protein; 25kD) |
| 2 | RC_N63772 | Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1; the ADORA2BP adenosine A2b receptor LIKE pseudogene; the IRF |
| 2 | RC_N63787 | ESTs |
| 2 | RC_N68168 | za11c1.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292224 3', mRNA sequence |
| 2 | RC_N68201 | ESTs; Weakly similar to hypothetical protein [H.sapiens] |
| 2 | RC_N68300 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 1 | RC_N68321 | solute carrier family 2 (facilitated glucose transporter); member 3 |
| 2 | RC_N69575 | EST |
| 2 | RC_N75007 | ESTs |
| 1 | RC_N75542 | ESTs |
| 2 | RC_N90066 | Homo sapiens clone 24689 mRNA sequence |
| 1 | RC_N91246 | ESTs |
| 1 | RC_N92751 | ESTs; Weakly similar to cyclic nucleotide-gated channel beta subunit [R.norvegicus] |
| 2 | RC_N93214_s | ESTs |
| 2 | RC_N99148 | ESTs; Highly similar to MKR2 PROTEIN [Mus musculus] |
| 4 | RC_R07876 | ESTs; Weakly similar to HYPOTHETICAL PROTEIN HI1723 [Haemophilus influenzae] |
| 1 | RC_R10865_f | alpha-fetoprotein |
| 2 | RC_R11056 | ESTs |
| 2 | RC_R11488 | ESTs |
| 1 | RC_R22947 | ESTs |
| 2 | RC_R23930_s | ESTs |
| 1 | RC_R26589_f | ESTs |
| 4 | RC_R37588_s | GDS-related protein |
| 2 | RC_R37613 | ESTs |
| 1 | RC_R38398 | Homo sapiens clone 23758 mRNA sequence |
| 2 | RC_R39179_f | ESTs |
| 1 | RC_R40923 | ESTs |
| 1 | RC_R41179 | Human mRNA for KIAA328 gene; partial cds |
| 2 | RC_R41294_s | ESTs |
| 1 | RC_R42307_f | early development regulator 2 (homolog of polyhomeotic 2) |
| 1 | RC_R43189_f | EST |
| 3 | RC_R43306 | ESTs |
| 1 | RC_R44357 | ESTs |
| 1 | RC_R44519 | EST; Moderately similar to Pro-Pol-dUTPase polyprotein [M.musculus] |
| 2 | RC_R45088 | yg38g4.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3', mRNA sequence |
| 2 | RC_R47948_i | ESTs |
| 1 | RC_R51524 | ESTs |
| 1 | RC_R54950 | ESTs |
| 1 | RC_R55241 | EST |
| 1 | RC_R59585 | ESTs |
| 1 | RC_R60044 | ESTs |
| 2 | RC_R60872 | ESTs |
| 1 | RC_R66690 | ESTs |
| 2 | RC_R67266_s | exostoses (multiple)-like 1 |
| 1 | RC_R73588 | ESTs |
| 3 | RC_R79403 | ESTs |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 1 | RC_R87647 | ESTs |
| 2 | RC_R93622 | ESTs |
| 4 | RC_R99599_s | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) |
| 4 | RC_R99612 | ESTs |
| 1 | RC_T02888 | FB14D6 Fetal brain, Stratagene Homo sapiens cDNA clone FB14D6 3'end, mRNA sequence |
| 1 | RC_T03170 | EST |
| 2 | RC_T10465 | hbc313 Human pancreatic islet Homo sapiens cDNA clone hbc313 3'end, mRNA sequence |
| 1 | RC_T15418_f | ESTs |
| 1 | RC_T15597_f | Homo sapiens mRNA for KIAA661 protein; complete cds |
| 2 | RC_T15652_i | ESTs |
| 2 | RC_T16898_s | ash2 (absent; small; or homeotic; Drosophila; homolog)-like |
| 1 | RC_T26644_i | ESTs; Weakly similar to zinc finger protein ZNF139 [H.sapiens] |
| 2 | RC_T40841 | ESTs |
| 1 | RC_T47566_i | yb15c11.s1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:71252 3' similar to similar to gb:Z2157 ELONGATION FACTOR 1-DELTA (HUMAN), mRNA sequence |
| 2 | RC_T50116 | ESTs; Moderately similar to EA22 GENE PROTEIN [Bacteriophage lambda] |
| 2 | RC_T50145_s | FSHD region gene 1 |
| 2 | RC_T58615 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] |
| 1 | RC_T59940_f | ESTs |
| 4 | RC_T63595 | ESTs |
| 2 | RC_T64891 | yd1c2.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66722 3', mRNA sequence |
| 2 | RC_T64924 | ESTs |
| 2 | RC_T64933_r | ESTs; Weakly similar to hypothetical protein [H.sapiens] |
| 2 | RC_T68875 | yc3f5.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:8229 3', mRNA sequence |
| 2 | RC_T69027 | ESTs |
| 3 | RC_T69924 | yc19d3.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:81125 3', mRNA sequence |
| 3 | RC_T70353 | ESTs |
| 1 | RC_T79780_s | ESTs; Weakly similar to PUTATIVE MITOCHONDRIAL CARRIER YBR291C [Saccharomyces cerevisiae] |
| 2 | RC_T79951 | ESTs |
| 3 | RC_T80174_s | ESTs |
| 3 | RC_T80622 | ESTs; Weakly similar to envelope protein RIC-7 [H.sapiens] |
| 1 | RC_T85352 | ESTs |
| 1 | RC_T85373 | ESTs |

| Cluster | Accession #/ PROBESET | Gene Description |
|---|---|---|
| 2 | RC_T86284 | ESTs; Weakly similar to transformation-related protein [H.sapiens] |
| 1 | RC_T89579_s | Homo sapiens E2F-related transcription factor (DP-1) mRNA; complete cds |
| 3 | RC_T90360 | ESTs |
| 2 | RC_T94328_i | ESTs |
| 1 | RC_T95590 | ye4a3.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:12172 3' similar to gb\|M1817\|IGURRAA Iguana iguana 5S (rRNA);, mRNA sequence |
| 4 | RC_T97257_f | ESTs; Weakly similar to hypothetical protein [H.sapiens] |
| 2 | RC_T97599_i | ESTs |
| 2 | RC_T97620 | ESTs; Weakly similar to unknown [H.sapiens] |
| 4 | RC_T97775 | ESTs |
| 3 | RC_T98152 | fibrillin 2 |
| 1 | RC_W31479 | ESTs |
| 1 | RC_W37999 | ESTs |
| 2 | RC_W38240 | Accession not listed in Genbank |
| 2 | RC_W40150 | human chromosome-associated polypeptide (bamacan) |
| 2 | RC_W45435 | Homo sapiens mRNA for KIAA784 protein; partial cds |
| 2 | RC_W58202 | ESTs |
| 1 | RC_W58344 | ESTs |
| 2 | RC_W58650 | ESTs |
| 4 | RC_W68736 | Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3; EC 1.6.99.3; CI-MLRQ); Tubulin Beta and Proto-oncogene Tyrosine-protein |
| 2 | RC_W69106 | ESTs |
| 2 | RC_W69111 | ESTs |
| 1 | RC_W69385_s | H.sapiens NuMA gene (Clone T33) |
| 3 | RC_W69399_s | ATPase; Ca++ transporting; plasma membrane 1 |
| 3 | RC_W69459 | ESTs |
| 2 | RC_W72424 | S1 calcium-binding protein A9 (calgranulin B) |
| 2 | RC_W72724 | ESTs |
| 2 | RC_W72834 | ESTs |
| 1 | RC_W73955 | Homo sapiens chromosome 19; cosmid R26445 |
| 2 | RC_W74701 | ESTs |
| 2 | RC_W76540 | ESTs |
| 2 | RC_W79397 | ESTs |
| 2 | RC_W85888 | ESTs; Weakly similar to synapse associated protein sap47-2 [D.melanogaster] |
| 2 | RC_W86038 | ESTs |
| 2 | RC_W86881 | ESTs |
| 2 | RC_W87804 | ESTs |
| 2 | RC_W88942 | zh7b5.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417393 3', mRNA sequence |

| Cluster | Accession # / PROBESET | Gene Description |
|---|---|---|
| 3 | RC_W90022 | ESTs; Highly similar to LECT2 precursor [H.sapiens] |
| 2 | RC_W92272 | Homo sapiens zinc-finger helicase (hZFH) mRNA; complete cds |
| 2 | RC_W92764_s | TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR |
| 2 | RC_W93040 | ESTs |
| 3 | RC_W93092 | neutral sphingomyelinase (N-SMase) activation associated factor |
| 2 | RC_W93227 | EST |
| 2 | RC_W93523 | ESTs |
| 2 | RC_W93659 | ESTs |
| 2 | RC_W94003_s | ESTs |
| 2 | RC_W94401_s | ESTs |
| 2 | RC_W94688 | Homo sapiens mRNA for perilipin; complete cds |
| 2 | RC_W94787_s | ESTs |
| 2 | RC_Z38294_s | ESTs |
| 3 | RC_Z38311 | ESTs |
| 2 | RC_Z38465_s | ESTs |
| 2 | RC_Z38525_s | ESTs |
| 2 | RC_Z38538_f | ESTs |
| 2 | RC_Z38551_s | ESTs |
| 2 | RC_Z38783_s | ca2+-dependent activator protein for secretion; Ca2+-regulated cytoskeletal protein (CAPS) |
| 2 | RC_Z39113 | ESTs |
| 4 | RC_Z39255_f | ESTs |
| 2 | RC_Z39591 | EST |
| 2 | RC_Z39783_s | ESTs |
| 2 | RC_Z39920 | ESTs; Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus] |
| 2 | RC_Z40166_f | ESTs |
| 3 | RC_Z40388_s | ESTs |
| 2 | RC_Z40646 | ESTs |
| 2 | RC_Z41697 | ESTs |
| 2 | RC_Z99349 | ESTs |
| 2 | RC_Z99394_s | ESTs; Weakly similar to transformation-related protein [H.sapiens] |

Table 2

| PROBESET | Example Accession | Complete/Title | SS2 (P3or) | TM2 (P3or) | MemType (P3or) | MemType (P3or) |
|---|---|---|---|---|---|---|
| EOS33789 | 1_U86782 | 26S proteasome-associated pad1 homolog | N | N | | N |
| EOS30212 | 1_X55740 | 5' nucleotidase (CD73) | Y | Y | Type Ia | YType Ia |
| EOS19489 | C_RC_W38197 | Accession not listed in Genbank | | | | |
| EOS33608 | 1_K02574 | Accession not listed in Genbank | | | | |
| EOS01114 | 1_L19871 | activating transcription factor 3 | N | N | | N |
| EOS33514 | 1_D90209 | activating transcription factor 4 (tax-responsive enha | N | N | | N |
| EOS00098 | 1_D14874 | adrenomedullin | Y | N | | N |
| EOS33456 | 1_M11313 | alpha-2-macroglobulin | Y | N | | N |
| EOS33029 | 1_L09209 | amyloid beta (A4) precursor-like protein 2 | N | N | | N |
| EOS01435 | 1_M27396 | asparagine synthetase | N | N | | N |
| EOS02429 | 1_U51478 | ATPase; Na+/K+ transporting; beta 3 polypeptide | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS06564 | A_RC_AA459916 | bradykinin receptor B2 | N | N | | N |
| EOS02490 | 1_U59289 | cadherin 13; H-cadherin (heart) | Y | Y | Type Ia | YType Ia |
| EOS01275 | 1_L76380 | calcitonin receptor-like | Y | Y | Type IIIa (clv | YType IIIa (clv) |
| EOS00459 | 1_HG1862-HT1897 | Calmodulin Type I | | | | |
| EOS30361 | 1_L10284 | calnexin | Y | Y | Type Ia | YType Ia |
| EOS01405 | 1_M23254 | calpain; large polypeptide L2 | N | N | | N |
| EOS24693 | D_RC_R39610_s | calpain; large polypeptide L2 | N | N | | N |
| EOS34311 | 1_U56637 | capping protein (actin filament) muscle Z-line; alpha | N | N | | N |
| EOS24656 | D_RC_R15740 | carbohydrate (chondroitin 6/keratan) sulfotransferas | Y | N | | N |
| EOS25539 | N_134_2 | carbohydrate (chondroitin 6/keratan) sulfotransferas | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS32648 | B_RC_T35289 | casein kinase 1; alpha 1 | N | N | | N |
| EOS01943 | 1_U03100 | catenin (cadherin-associated protein); alpha 1 (102k | N | N | | N |
| EOS03277 | 1_X87838 | catenin (cadherin-associated protein); beta 1 (88kD) | N | N | | N |
| EOS00780 | 1_HG417-HT417 | Cathepsin B | | | | |
| EOS34488 | 1_S53911 | CD34 | Y | Y | Type Ia | YType Ia |
| EOS01723 | 1_M84349 | CD59 antigen p18-20 (antigen identified by monoclo | Y | N | | N |
| EOS34423 | 1_X15183 | CDW52 antigen (CAMPATH-1 antigen) | N | N | | N |
| EOS01027 | 1_L06797 | chemokine (C-X-C motif); receptor 4 (fusin) | N | Y | Type IIIb (Ne | YType IIIb (Nexo Ccyt) |
| EOS00548 | 1_HG2614-HT2710 | Collagen, Type Viii, Alpha 1 | | | | |
| EOS01426 | 1_M26576_cds2 | collagen; type IV; alpha 1 | Y | N | | N |
| EOS01768 | 1_M92934 | connective tissue growth factor | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS29428 | D_RC_AA449789_f | connective tissue growth factor | | | | |
| EOS03010 | 1_X59798 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | N | N | | N |

**Table 2, cont.**

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS33328 | 1_X02612 | cytochrome P450; subfamily I (aromatic compound-i | Y | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS24269 | D_RC_H99093 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72kD) | | | | |
| EOS02890 | 1_X15729 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 ( | N | N | | N |
| EOS01896 | 1_S81914 | DIFFERENTIATION-DEPENDENT GENE 2 | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS33581 | 1_U97105 | dihydropyrimidinase-like 2 | N | N | | N |
| EOS34133 | 1_M60278 | diphtheria toxin receptor (heparin-binding epidermal | Y | Y | Type Ia | YType Ia |
| EOS34269 | A_RC_AA478971_s | disabled (Drosophila) homolog 2 (mitogen-responsiv | N | N | | N |
| EOS29195 | 1_X68277 | dual specificity phosphatase 1 | N | N | | N |
| EOS32233 | C_RC_AA620962 | dynein; cytoplasmic; light intermediate polypeptide 2 | Y | N | | N |
| EOS02230 | 1_U32944 | dynein; cytoplasmic; light polypeptide | N | N | | N |
| EOS02941 | 1_X52541 | early growth response 1 | N | N | | N |
| EOS01954 | 1_U03877 | EGF-containing fibulin-like extracellular matrix protei | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS31010 | 1_J05008 | endothelin 1 | Y | N | | N |
| EOS28572 | 1_L35240 A_L3524 | enigma (LIM domain protein) | N | N | | N |
| EOS01563 | 1_M57730 | ephrin-A1 | Y | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS03897 | A_AA303711 | ephrin-B1 | Y | Y | Type Ia | YType Ia |
| EOS21265 | D_RC_AA404418 | EST | | | | |
| EOS04377 | A_L44538 | ESTs | N | N | | N |
| EOS04694 | A_RC_AA025351 | ESTs | N | N | | N |
| EOS04713 | A_RC_AA027050 | ESTs | Y | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS04728 | A_RC_AA029462 | ESTs | N | N | | N |
| EOS04795 | A_RC_AA045136 | ESTs | N | N | | N |
| EOS04807 | A_RC_AA047437 | ESTs | N | N | | N |
| EOS05108 | A_RC_AA187490 | ESTs | N | N | | N |
| EOS05145 | A_RC_AA205724 | ESTs | N | N | | N |
| EOS05193 | A_RC_AA227926 | ESTs | N | N | | N |
| EOS05201 | A_RC_AA227986 | ESTs | N | N | | N |
| EOS05260 | A_RC_AA234743 | ESTs | N | N | | N |
| EOS05391 | A_RC_AA253216 | ESTs | N | N | | N |
| EOS05423 | A_RC_AA256268 | ESTs | N | N | | N |
| EOS05697 | A_RC_AA346551 | ESTs | N | N | | N |
| EOS05812 | A_RC_AA400292 | ESTs | N | N | | N |
| EOS05866 | A_RC_AA404338 | ESTs | N | N | | N |
| EOS06054 | A_RC_AA423987 | ESTs | N | N | | N |
| EOS06152 | A_RC_AA428594 | ESTs | N | N | | N |

Table 2, cont.

| | | | | | |
|---|---|---|---|---|---|
| EOS06171 | A_RC_AA430108 | ESTs | N | N | N |
| EOS06193 | A_RC_AA431462 | ESTs | N | N | N |
| EOS06654 | A_RC_AA465226 | ESTs | N | N | N |
| EOS06723 | A_RC_AA478778 | ESTs | N | N | N |
| EOS06729 | A_RC_AA479037 | ESTs | Y | N | N |
| EOS06891 | A_RC_AA504110 | ESTs | N | N | N |
| EOS06960 | A_RC_AA599434 | ESTs | N | Y | Type II (Ncyt YType II (Ncyt Cexo) |
| EOS07016 | A_RC_AA609519 | ESTs | N | N | N |
| EOS08437 | B_RC_AA083514 | ESTs | N | Y | Type II (Ncyt YType II (Ncyt Cexo) |
| EOS08625 | B_RC_AA121315 | ESTs | Y | N | N |
| EOS08861 | B_RC_AA147186 | ESTs | | | |
| EOS08931 | B_RC_AA156125 | ESTs | N | N | N |
| EOS09125 | B_RC_AA188932 | ESTs | N | N | N |
| EOS09320 | B_RC_AA219653 | ESTs | N | N | N |
| EOS09386 | B_RC_AA232645 | ESTs | N | N | N |
| EOS09667 | B_RC_F10078 | ESTs | N | N | N |
| EOS10341 | B_RC_H48032 | ESTs | N | N | N |
| EOS10590 | B_RC_H82117 | ESTs | N | N | N |
| EOS10836 | B_RC_N39584 | ESTs | N | N | N |
| EOS11021 | B_RC_N59858 | ESTs | N | N | N |
| EOS11286 | B_RC_N90933 | ESTs | Y | N | N |
| EOS11671 | B_RC_R26124 | ESTs | N | N | N |
| EOS11699 | B_RC_R27957 | ESTs | N | N | N |
| EOS13420 | B_RC_T88700 | ESTs | N | N | N |
| EOS13472 | B_RC_T90527 | ESTs | N | N | N |
| EOS13733 | B_RC_W42789 | ESTs | N | N | N |
| EOS13840 | B_RC_W78175 | ESTs | N | N | N |
| EOS13877 | B_RC_W84768 | ESTs | | | |
| EOS14991 | C_RC_AA253217 | ESTs | N | N | N |
| EOS15749 | C_RC_AA426573 | ESTs | N | Y | Type II (Ncyt YType II (Ncyt Cexo) |
| EOS15800 | C_RC_AA432374 | ESTs | N | N | N |
| EOS15894 | C_RC_AA446622 | ESTs | N | N | N |
| EOS16158 | C_RC_AA478771 | ESTs | N | N | N |
| EOS16194 | C_RC_AA482594 | ESTs | N | N | N |
| EOS16244 | C_RC_AA490588 | ESTs | N | N | N |

**Table 2, cont.**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| EOS16519 | C_RC_D59570_f | ESTs | Y | Y | Type II (Ncyt Y | Type II (Ncyt Cexo) | | | | |
| EOS16953 | C_RC_H88157 | ESTs | N | Y | Type II (Ncyt Y | Type II (Ncyt Cexo) | | | | |
| EOS17042 | C_RC_H94648 | ESTs | N | N | N | | | | | |
| EOS17086 | C_RC_H97538 | ESTs | N | N | N | | | | | |
| EOS20585 | D_RC_AA287347 | ESTs | N | N | N | | | | | |
| EOS21244 | D_RC_AA402799 | ESTs | N | N | N | | | | | |
| EOS21752 | D_RC_AA425107 | ESTs | N | N | N | | | | | |
| EOS22261 | D_RC_AA442872 | ESTs | Y | N | N | | | | | |
| EOS23989 | D_RC_F13673 | ESTs | N | N | N | | | | | |
| EOS25097 | D_RC_W45560 | ESTs | N | N | N | | | | | |
| EOS25237 | D_RC_Z40583_f | ESTs | N | N | N | | | | | |
| EOS25259 | N_101234_4 | ESTs | N | Y | Type II (Ncyt Y | Type II (Ncyt Cexo) | | | | |
| EOS27365 | N_62063_2 | ESTs | N | N | N | | | | | |
| EOS27496 | N_665011_1 | ESTs | N | Y | Type Ib (Nex Y | Type Ib (Nexo Ccyt) | | | | |
| EOS27549 | N_682558_1 | ESTs | N | N | N | | | | | |
| EOS28833 | A_R69417 | ESTs | N | N | N | | | | | |
| EOS29017 | B_RC_N72695_s | ESTs | N | N | N | | | | | |
| EOS29418 | A_AA228107 | ESTs | N | N | N | | | | | |
| EOS29487 | A_W01367_s B_RC | ESTs | | N | N | | | | | |
| EOS30568 | C_RC_H16402 | ESTs | N | N | Type II (Ncyt Y | Type II (Ncyt Cexo) | | | | |
| EOS30569 | C_RC_D59711_f | ESTs | Y | Y | N | | | | | |
| EOS30616 | A_RC_AA431571 | ESTs | N | N | N | | | | | |
| EOS30748 | A_RC_AA280375 C | ESTs | N | N | N | | | | | |
| EOS30829 | B_RC_Z41740_s | ESTs | N | N | N | | | | | |
| EOS31014 | A_RC_AA101878 | ESTs | Y | N | N | | | | | |
| EOS31037 | A_N87590 | ESTs | N | N | N | | | | | |
| EOS31112 | A_RC_AA256153_I | ESTs | N | N | N | | | | | |
| EOS31494 | A_RC_AA491465 | ESTs | N | N | N | | | | | |
| EOS31503 | A_AA046593 A_RC | ESTs | N | N | N | | | | | |
| EOS31686 | A_D45304 D_RC_N | ESTs | N | N | N | | | | | |
| EOS31976 | A_AA384503_s | ESTs | N | N | N | | | | | |
| EOS31980 | A_AA136353 | ESTs | N | N | N | | | | | |
| EOS32328 | A_R31641 | ESTs | N | N | N | | | | | |
| EOS32351 | C_RC_AA489190 | ESTs | Y | Y | Type Ib (Nex Y | Type Ib (Nexo Ccyt) | | | | |
| EOS32813 | A_AA047151 A_RC | ESTs | N | N | N | | | | | |

**Table 2, cont.**

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| EOS32919 | A_AA480074 | ESTs | N | N | | | N | | |
| EOS33001 | B_RC_T99789 | ESTs | N | N | | | N | | |
| EOS33079 | B_RC_T16484_s | ESTs | N | N | | | N | | |
| EOS33091 | A_RC_AA253193 | ESTs | Y | N | | | N | | |
| EOS33130 | A_RC_AA432248 D | ESTs | N | N | | | N | | |
| EOS33279 | A_N75791_s A_RC | ESTs | N | N | | | N | | |
| EOS33440 | B_RC_AA227913 C | ESTs | N | N | | | N | | |
| EOS33819 | A_AA099391_s B_ | ESTs | N | N | | | N | | |
| EOS34229 | A_RC_AA487558 A | ESTs | N | N | | | N | | |
| EOS34992 | A_AA174183_s | ESTs | N | N | | | N | | |
| EOS35003 | A_AA452000 C_RC | ESTs | N | N | | | N | | |
| EOS35100 | A_RC_AA282140 A | ESTs | N | N | | | N | | |
| EOS31845 | A_AA316186 A_RC | ESTs; Highly similar to (defline not available 426213 | N | N | | | N | | |
| EOS29549 | A_RC_AA610116_1 | ESTs; Highly similar to (defline not available 432518 | N | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) | | | |
| EOS31021 | A_T35341_s | ESTs; Highly similar to (defline not available 451988 | N | N | | | N | | |
| EOS06772 | A_RC_AA482597 | ESTs; Highly similar to (defline not available 470473 | N | N | | | N | | |
| EOS06384 | A_RC_AA449479 | ESTs; Highly similar to (defline not available 510678 | Y | N | | | N | | |
| EOS06798 | A_RC_AA487561 | ESTs; Highly similar to RAS-RELATED PROTEIN R | N | N | | | N | | |
| EOS06904 | A_RC_AA520989 | ESTs; Highly similar to SERINE/THREONINE PRO | N | N | | | N | | |
| EOS28445 | A_RC_AA149044 | ESTs; Highly similar to the KIAA0195 gene is expre | Y | N | | | N | | |
| EOS12881 | B_RC_T16550 | ESTs; Highly similar to vacuolar protein sorting hom | N | N | | | N | | |
| EOS11308 | B_RC_N93784 | ESTs; Moderately similar to !!!! ALU CLASS C WAR | Y | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) | | | |
| EOS21765 | D_RC_AA425435 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J | N | N | | | N | | |
| EOS19796 | C_RC_W80814 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | N | N | | | N | | |
| EOS04882 | A_RC_AA071089 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | Y | N | | | N | | |
| EOS17210 | C_RC_N22107 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | N | N | | | N | | |
| EOS22507 | D_RC_AA452860 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | N | N | | | N | | |
| EOS05657 | A_RC_AA292379 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | N | N | | | N | | |
| EOS23090 | D_RC_AA488687 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | Y | N | | | N | | |
| EOS06296 | A_RC_AA443756 | ESTs; Moderately similar to (defline not available 41 | N | N | | | N | | |
| EOS28553 | A_D78676 D_RC_A | ESTs; Moderately similar to (defline not available 45 | N | N | | | N | | |
| EOS05524 | A_RC_AA279397 | ESTs; Moderately similar to fibronectin [H.sapiens] | N | N | | | N | | |
| EOS12248 | B_RC_R55470 | ESTs; Moderately similar to K02E10.2 [C.elegans] | N | N | | | N | | |
| EOS05126 | A_RC_AA195031 | ESTs; Moderately similar to PROBABLE G PROTEI | N | N | | | N | | |
| EOS34919 | A_AA236324 B_RC | ESTs; Weakly similar to !!!! ALU CLASS A WARNIN | Y | N | | | N | | |

Table 2, cont.

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS34999 | C_RC_AA456311_s | ESTs; Weakly similar to !!!! ALU CLASS A WARNIN | Y | N | | N |
| EOS32081 | A_AA044755_s D_ | ESTs; Weakly similar to !!!! ALU SUBFAMILY SX W | N | N | | N |
| EOS17106 | C_RC_H98670 | ESTs; Weakly similar to (defline not available 48840 | N | N | | N |
| EOS06194 | A_RC_AA431470 | ESTs; Weakly similar to CAMP-DEPENDENT PRO | N | N | | N |
| EOS28844 | A_AA232837 | ESTs; Weakly similar to Human pre-mRNA cleavag | Y | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS05662 | A_RC_AA292717 | ESTs; Weakly similar to JM2 [H.sapiens] | N | N | | N |
| EOS32117 | A_RC_AA058911 | ESTs; Weakly similar to membrane glycoprotein [M. | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS13977 | B_RC_W94427 | ESTs; Weakly similar to Na;K-ATPase gamma subu | Y | Y | Type Ia | YType Ia |
| EOS12987 | B_RC_T26674 | ESTs; Weakly similar to neuronal thread protein AD | N | N | | N |
| EOS23416 | D_RC_AA599674 | ESTs; Weakly similar to ORF [D.melanogaster] | N | N | | N |
| EOS32540 | A_RC_AA443114 | ESTs; Weakly similar to PIM-1 PROTO-ONCOGEN | N | N | | N |
| EOS05043 | A_RC_AA156450 | ESTs; Weakly similar to Similar to Rat trg gene prod | N | N | | N |
| EOS06820 | A_RC_AA489245 | ESTs; Weakly similar to sperm specific protein [H.sapiens] | | | | |
| EOS31839 | D_RC_W69127_s | ESTs; Weakly similar to zinc finger protein ZNF191 [ | N | N | | N |
| EOS03125 | 1_X70940 | eukaryotic translation elongation factor 1 alpha 2 | N | N | | N |
| EOS02623 | 1_U73824 | eukaryotic translation initiation factor 4 gamma; 2 | N | N | | N |
| EOS01787 | 1_M94856 | fatty acid binding protein 5 (psoriasis-associated) | N | N | | N |
| EOS28383 | 1_X02761 | fibronectin 1 | N | N | | N |
| EOS00606 | 1_HG3044-HT3742 | Fibronectin, Alt. Splice 1 | | | | |
| EOS02950 | 1_X53416 | filamin A; alpha (actin-binding protein-280) | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS01612 | 1_M62994 | filamin B; beta (actin-binding protein-278) | N | N | | N |
| EOS01247 | 1_L42176 | four and a half LIM domains 2 | N | N | | N |
| EOS33732 | 1_L16862 A_RC_A | G protein-coupled receptor kinase 6 | N | N | | N |
| EOS33447 | 1_X52947 | gap junction protein; alpha 1; 43kD (connexin 43) | N | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |
| EOS02812 | 1_X04412 | gelsolin (amyloidosis; Finnish type) | N | N | | N |
| EOS02959 | 1_X54489_ma1 | GRO1 oncogene (melanoma growth stimulating acti | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS01564 | 1_M57731 | GRO2 oncogene | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS02213 | 1_U31384 | guanine nucleotide binding protein 11 | N | N | | N |
| EOS33321 | 1_X57579 C_RC_N | H.sapiens activin beta-A subunit (exon 2) | Y | N | | N |
| EOS33408 | A_X83703 D_RC_A | H.sapiens mRNA for cytokine inducible nuclear prot | N | N | | N |
| EOS25234 | D_RC_Z39833 | H.sapiens mRNA for Rho6 protein | N | N | | N |
| EOS33601 | D_RC_T25747_s | H.sapiens OZF mRNA | | | | |
| EOS03362 | 1_X97748 | H.sapiens PTX3 gene promotor region | | | | |
| EOS03068 | 1_X65965 | H.sapiens SOD-2 gene for manganese superoxide dismutase | | | | |
| EOS32288 | 1_X60486 | H4 histone family; member G | N | N | | N |

Table 2, cont.

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS00588 | 1_HG2855-HT2995 | Heat Shock Protein, 70 Kda (Gb:Y00371) | | | | |
| EOS35001 | 1_L08069 | heat shock protein; DNAJ-like 2 | N | N | | N |
| EOS02837 | 1_X06985 | heme oxygenase (decycling) 1 | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS01674 | 1_M75126 | hexokinase 1 | N | N | | N |
| EOS01487 | 1_M31994 | Homo sapiens aldehyde dehydrogenase (ALDH1) gene, exon 13 and complete cds | | | | |
| EOS32770 | A_N23817 A_RC_A | Homo sapiens clone 23675 mRNA sequence | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS33421 | 1_L40395 A_L4039 | Homo sapiens clone 23689 mRNA; complete cds | N | N | | N |
| EOS06991 | A_RC_AA608649 | Homo sapiens clone 23742 mRNA; partial cds | Y | Y | Type Ia | YType Ia |
| EOS02519 | 1_U62015 | Homo sapiens Cyr61 mRNA, complete cds | Y | N | | N |
| EOS00044 | 1_D00596 | Homo sapiens gene for thymidylate synthase; exons | N | N | | N |
| EOS33755 | 1_U44975 | Homo sapiens Kruppel-like zinc finger protein Zf9 m | N | N | | N |
| EOS34982 | B_RC_AA148923 | Homo sapiens mRNA for DEPP (decidual protein in | N | N | | N |
| EOS29692 | A_RC_AA460273 A | Homo sapiens mRNA for KIAA0517 protein; partial c | N | N | | N |
| EOS30706 | A_R79356 | Homo sapiens mRNA for KIAA0544 protein; partial c | N | N | | N |
| EOS30932 | A_RC_AA121543 D | Homo sapiens mRNA for KIAA0758 protein; partial c | Y | N | | N |
| EOS31137 | B_RC_W74533 D_ | Homo sapiens mRNA for KIAA0786 protein; partial c | Y | N | | N |
| EOS32898 | A_N77151 C_RC_A | Homo sapiens mRNA for KIAA0799 protein; partial c | N | N | | N |
| EOS00335 | 1_D86425 | Homo sapiens mRNA for nidogen-2 | Y | N | | N |
| EOS10948 | B_RC_N54067 | Homo sapiens mRNA for NIK; partial cds | | | | |
| EOS07915 | B_RC_AA035638 | Homo sapiens mRNA; cDNA DKFZp564F053 (from | Y | N | | N |
| EOS25528 | N_132515_1 | Homo sapiens mRNA; cDNA DKFZp564F053 (from | Y | N | | N |
| EOS29557 | A_RC_AA258308 | Homo sapiens mRNA; cDNA DKFZp564F053 (from | Y | N | | N |
| EOS02390 | 1_U48959 | Homo sapiens myosin light chain kinase (MLCK) m | N | N | | N |
| EOS34333 | 1_M61199 | Human cleavage signal 1 protein mRNA; complete c | N | N | | N |
| EOS02617 | 1_U73379 | Human cyclin-selective ubiquitin carrier protein mRN | N | N | | N |
| EOS34005 | 1_U28811 | Human cysteine-rich fibroblast growth factor recepto | N | N | | N |
| EOS01098 | 1_L15388 | Human G protein-coupled receptor kinase (GRK5) | N | N | | N |
| EOS01266 | 1_L49169 | Human G0S3 mRNA; complete cds | N | N | | N |
| EOS02530 | 1_U63825 | Human hepatitis delta antigen interacting protein A ( | N | N | | N |
| EOS33492 | 1_M60721 | Human homeobox gene, complete cds | Y | N | | N |
| EOS07146 | A_RC_D51069_f | Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds | | | | |
| EOS01122 | 1_L20859 | Human leukemia virus receptor 1 (GLVR1) mRNA; c | N | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |
| EOS02575 | 1_U67963 | Human lysophospholipase homolog (HU-K5) mRNA; | N | N | | N |
| EOS02325 | 1_U41767 | Human metargidin precursor mRNA, complete cds | Y | Y | Type Ia | YType Ia |
| EOS33547 | A_RC_AA148318_s | Human mRNA for KIAA0069 gene; partial cds | N | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |

Table 2, cont.

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS31622 | 1_D50914 | Human mRNA for KIAA0124 gene; partial cds | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS00350 | 1_D86983 | Human mRNA for KIAA0230 gene; partial cds | Y | N | | N |
| EOS34346 | 1_M28882 1_X6826 | Human MUC18 glycoprotein mRNA, complete cds | Y | Y | Type Ia | YType Ia |
| EOS02421 | 1_U51010 | Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region | | | | |
| EOS02453 | 1_U53445 | Human ovarian cancer downregulated myosin heavy N | | N | | N |
| EOS01644 | 1_M68874 | Human phosphatidylcholine 2-acylhydrolase (cPLA2 N | | N | | N |
| EOS02308 | 1_U40369_ma1 | Human spermidine/spermine N1-acetyltransferase ( N | | N | | N |
| EOS34747 | 1_U20734 1_X5134 | Human transcription factor junB (junB) gene; 5' regio N | | N | | N |
| EOS00648 | 1_HG3342-HT3519 | Id1 | | | | |
| EOS33368 | D_RC_H44631_s | immediate early protein | N | N | | N |
| EOS29156 | 1_M96843 A_M968 | inhibitor of DNA binding 2; dominant negative helix-l N | | N | | N |
| EOS33768 | 1_M97796 | inhibitor of DNA binding 2; dominant negative helix-l N | | N | | N |
| EOS03108 | 1_X69111 | inhibitor of DNA binding 3; dominant negative helix-l N | | N | | N |
| EOS02986 | 1_X57206 | inositol 1;4;5-trisphosphate 3-kinase B | N | N | | N |
| EOS00682 | 1_HG3543-HT3739 | Insulin-Like Growth Factor 2 | | | | |
| EOS01517 | 1_M35878 | insulin-like growth factor binding protein 3 | Y | N | | N |
| EOS30108 | 1_M62403 | insulin-like growth factor-binding protein 4 | Y | N | | N |
| EOS32476 | 1_M24283 B_RC_A | intercellular adhesion molecule 1 (CD54); human rhi Y | | Y | Type Ia | YType Ia |
| EOS01490 | 1_M32334 | intercellular adhesion molecule 2 | Y | Y | Type Ia | YType Ia |
| EOS31485 | A_RC_AA161292_s | interferon; alpha-inducible protein 27 | N | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |
| EOS33077 | 1_D12763 | interleukin 1 receptor-like 1 | Y | N | | N |
| EOS32929 | 1_Y00787 | interleukin 8 | Y | N | | N |
| EOS32450 | C_RC_AA257993 | Janus kinase 1 (a protein tyrosine kinase) | N | N | | N |
| EOS31439 | 1_X56681 | jun D proto-oncogene | N | N | | N |
| EOS02857 | 1_X12876 | keratin 18 | N | N | | N |
| EOS34262 | 1_D86962 | KIAA0207 gene product | N | N | | N |
| EOS02689 | 1_U81607 | kinase scaffold protein gravin | N | N | | N |
| EOS28599 | D_RC_AA598737_s | lactate dehydrogenase B | Y | N | | N |
| EOS33969 | 1_S78569 | laminin; alpha 4 | Y | N | | N |
| EOS32420 | B_RC_F13782_s C | LIM binding domain 2 | N | N | | N |
| EOS33225 | 1_L00352 | low density lipoprotein receptor (familial hypercholes Y | | Y | Type Ia | YType Ia |
| EOS29814 | A_RC_AA286710 | lymphocyte adaptor protein | N | N | | N |
| EOS02734 | 1_U89942 | lysyl oxidase-like 2 | Y | N | | N |
| EOS02494 | 1_U59423 | MAD (mothers against decapentaplegic; Drosophila) N | | N | | N |
| EOS28425 | A_AF010193 | MAD (mothers against decapentaplegic; Drosophila) N | | N | | N |

Table 2, cont.

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS00073 | 1_D13640 | major histocompatibility complex; class I; C | N | N | | N |
| EOS33652 | 1_X53331 | matrix Gla protein | Y | N | | N |
| EOS02966 | 1_X54925 | matrix metalloproteinase 1 (interstitial collagenase) | Y | N | | N |
| EOS02845 | 1_X07820 | matrix metalloproteinase 10 (stromelysin 2) | Y | N | | N |
| EOS29948 | B_RC_T68873_f | metallothionein 1L | N | N | | N |
| EOS02639 | 1_U77604 | microsomal glutathione S-transferase 2 | Y | Y | Type Ia | YType Ia |
| EOS00758 | 1_HG4069-HT4339 | Monocyte Chemotactic Protein 1 | | | | |
| EOS01040 | 1_L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | Y | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS29275 | A_AA292440_s D_ | myeloid differentiation primary response | N | N | | N |
| EOS02051 | 1_U14391 | myosin IC | N | N | | N |
| EOS35126 | 1_J02854 | myosin regulatory light chain 2; smooth muscle isofo | N | N | | N |
| EOS24294 | D_RC_N23031 | myosin; heavy polypeptide 7; cardiac muscle; beta | N | N | | N |
| EOS34094 | D_RC_C14407_f D_ | neuronal tissue-enriched acidic protein | N | N | | N |
| EOS01989 | 1_U08021 | nicotinamide N-methyltransferase | N | N | | N |
| EOS00385 | 1_D87953 | N-myc downstream regulated | N | N | | N |
| EOS01650 | 1_M69043 | nuclear factor of kappa light polypeptide gene enhan | N | N | | N |
| EOS01597 | 1_M60858_rna1 | nucleolin | N | N | | N |
| EOS05422 | A_RC_AA256210 | oncomodulin | N | N | | N |
| EOS30077 | 1_D63476 | PAK-interacting exchange factor beta | N | N | | N |
| EOS01473 | 1_M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | Y | N | | N |
| EOS00060 | 1_D11428 | peripheral myelin protein 22 | Y | Y | Type IIIa (clv | YType IIIa (clv) |
| EOS04824 | A_RC_AA054087 | phospholipase A2; group IVC (cytosolic; calcium-ind | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS35278 | A_AA442054_s | phospholipase C; gamma 1 (formerly subtype 148) | Y | N | | N |
| EOS33907 | 1_L19314 | phosphorylase kinase; beta | N | N | | N |
| EOS30483 | A_RC_AA430032 | pituitary tumor-transforming 1 | N | N | | N |
| EOS00921 | 1_J03764 | plasminogen activator inhibitor; type I | N | N | | N |
| EOS13777 | B_RC_W60002_s | plastin 3 (T isoform) | N | N | | N |
| EOS07315 | A_U97519 | podocalyxin-like | N | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |
| EOS05961 | A_RC_AA412284_s | poliovirus receptor | Y | N | | N |
| EOS01522 | 1_M36429 | postmeiotic segregation increased 2-like 12 | N | N | | N |
| EOS32094 | 1_U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (ly | N | N | | N |
| EOS07374 | A_W28391 | proliferation-associated 2G4; 38kD | N | N | | N |
| EOS01086 | 1_L13977 | prolylcarboxypeptidase (angiotensinase C) | Y | N | | N |
| EOS34913 | 1_D28235 1_U0463 | prostaglandin-endoperoxide synthase 2 (prostagland | Y | N | | N |
| EOS01770 | 1_M93056 | protease inhibitor 2 (anti-elastase); monocyte/neutro | N | Y | Type Ib (Nex | YType Ib (Nexo C |

**Table 2, cont.**

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS00073 | 1_D13640 | major histocompatibility complex; class I; C | N | N | | N |
| EOS33652 | 1_X53331 | matrix Gla protein | Y | N | | N |
| EOS02966 | 1_X54925 | matrix metalloproteinase 1 (interstitial collagenase) | Y | N | | N |
| EOS02845 | 1_X07820 | matrix metalloproteinase 10 (stromelysin 2) | Y | N | | N |
| EOS29948 | B_RC_T68873_f | metallothionein 1L | N | N | | N |
| EOS02639 | 1_U77604 | microsomal glutathione S-transferase 2 | Y | Y | Type Ia | YType Ia |
| EOS00758 | 1_HG4069-HT4339 | Monocyte Chemotactic Protein 1 | | | | |
| EOS01040 | 1_L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | Y | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS29275 | A_AA292440_s D_ | myeloid differentiation primary response | N | N | | N |
| EOS02051 | 1_U14391 | myosin IC | N | N | | N |
| EOS35126 | 1_J02854 | myosin regulatory light chain 2; smooth muscle isofo | N | N | | N |
| EOS24294 | D_RC_N23031 | myosin; heavy polypeptide 7; cardiac muscle; beta | N | N | | N |
| EOS34094 | D_RC_C14407_f D_ | neuronal tissue-enriched acidic protein | N | N | | N |
| EOS01989 | 1_U08021 | nicotinamide N-methyltransferase | N | N | | N |
| EOS00385 | 1_D87953 | N-myc downstream regulated | N | N | | N |
| EOS01650 | 1_M69043 | nuclear factor of kappa light polypeptide gene enhan | N | N | | N |
| EOS01597 | 1_M60858_ma1 | nucleolin | N | N | | N |
| EOS05422 | A_RC_AA256210 | oncomodulin | N | N | | N |
| EOS30077 | 1_D63476 | PAK-interacting exchange factor beta | N | N | | N |
| EOS01473 | 1_M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | Y | N | | N |
| EOS00060 | 1_D11428 | peripheral myelin protein 22 | Y | Y | Type IIIa (clv | YType IIIa (clv) |
| EOS04824 | A_RC_AA054087 | phospholipase A2; group IVC (cytosolic; calcium-ind | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS35278 | A_AA442054_s | phospholipase C; gamma 1 (formerly subtype 148) | Y | N | | N |
| EOS33907 | 1_L19314 | phosphorylase kinase; beta | N | N | | N |
| EOS30483 | A_RC_AA430032 | pituitary tumor-transforming 1 | N | N | | N |
| EOS00921 | 1_J03764 | plasminogen activator inhibitor; type I | N | N | | N |
| EOS13777 | B_RC_W60002_s | plastin 3 (T isoform) | N | N | | N |
| EOS07315 | A_U97519 | podocalyxin-like | N | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |
| EOS05961 | A_RC_AA412284_s | poliovirus receptor | Y | N | | N |
| EOS01522 | 1_M36429 | postmeiotic segregation increased 2-like 12 | N | N | | N |
| EOS32094 | 1_U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (ly | N | N | | N |
| EOS07374 | A_W28391 | proliferation-associated 2G4; 38kD | N | N | | N |
| EOS01086 | 1_L13977 | prolylcarboxypeptidase (angiotensinase C) | Y | N | | N |
| EOS34913 | 1_D28235 1_U0463 | prostaglandin-endoperoxide synthase 2 (prostagland | Y | N | | N |
| EOS01770 | 1_M93056 | protease inhibitor 2 (anti-elastase); monocyte/neutro | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |

Table 2, cont.

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS01861 | 1_S76965 | Protein kinase inhibitor [human; neuroblastoma cell l | N | N | | N |
| EOS03401 | 1_Y00815 | protein tyrosine phosphatase; receptor type; F | Y | N | | N |
| EOS34011 | 1_L77886 | protein tyrosine phosphatase; receptor type; K | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS00138 | 1_D26129 | ribonuclease; RNase A family; 1 (pancreatic) | Y | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS30425 | D_RC_AA243278_i | ribosomal protein; mitochondrial; L12 | N | N | | N |
| EOS29398 | 1_J03040 | secreted protein; acidic; cysteine-rich (osteonectin) | Y | N | | N |
| EOS01415 | 1_M24736 | selectin E (endothelial adhesion molecule 1) | Y | Y | Type Ia | YType Ia |
| EOS01942 | 1_U03057 | singed (Drosophila)-like (sea urchin fascin homolog l | N | N | | N |
| EOS00549 | 1_HG2639-HT2735 | Single-Stranded Dna-Binding Protein Mssp-1 | | | | |
| EOS32244 | A_AA285290 | small EDRK-rich factor 2 | N | N | | N |
| EOS30770 | 1_Z49269 | small inducible cytokine subfamily A (Cys-Cys); me | Y | N | | N |
| EOS28510 | 1_U82108 | solute carrier family 9 (sodium/hydrogen exchanger) | N | N | | N |
| EOS34168 | C_RC_R81509_s | splicing factor; arginine/serine-rich 11 | N | N | | N |
| EOS31249 | 1_U25997 | stanniocalcin | N | N | | N |
| EOS33150 | 1_X82200 | stimulated trans-acting factor (50 kDa) | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS33384 | A_AA090257 D_RC | superoxide dismutase 2; mitochondrial | | | | |
| EOS03301 | 1_X91247 | thioredoxin reductase 1 | N | N | | N |
| EOS00154 | 1_D28476 | thyroid hormone receptor interactor 12 | N | N | | N |
| EOS33468 | 1_L14837 | tight junction protein 1 (zona occludens 1) | N | N | | N |
| EOS33905 | 1_D29992 1_L2762 | tissue factor pathway inhibitor 2 | Y | N | | N |
| EOS33006 | B_RC_W84341 | tissue inhibitor of metalloproteinase 2 | N | N | | N |
| EOS01671 | 1_M74719 | transcription factor 4 | N | N | | N |
| EOS34273 | 1_D50683 | transforming growth factor; beta receptor II (70-80kD | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS01794 | 1_M95787 | transgelin | N | N | | N |
| EOS01072 | 1_L12711 | transketolase (Wernicke-Korsakoff syndrome) | N | N | | N |
| EOS31789 | 1_M90657 | transmembrane 4 superfamily member 1 | Y | Y | Type IIIa (clv | YType IIIa (clv) |
| EOS33890 | 1_M19267 1_Z2472 | tropomyosin 1 (alpha) | N | N | | N |
| EOS33611 | 1_D78577 | tyrosine 3-monooxygenase/tryptophan 5-monooxyg | N | N | | N |
| EOS03025 | 1_X60957 | tyrosine kinase with immunoglobulin and epidermal | Y | N | | N |
| EOS33660 | 1_S73591 D_RC_N | upregulated by 1;25-dihydroxyvitamin D-3 | N | N | | N |
| EOS29118 | 1_M30257 A_M732 | vascular cell adhesion molecule 1 | Y | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |
| EOS31258 | 1_V01512_ma1 | v-fos FBJ murine osteosarcoma viral oncogene hom | N | N | | N |
| EOS33190 | A_AA083572 A_RC | v-ral simian leukemia viral oncogene homolog A (ras | N | N | | N |
| EOS01330 | 1_M15990 | v-yes-1 Yamaguchi sarcoma viral oncogene homolo | N | N | | N |
| EOS13125 | B_RC_T57112 | yc20g11.s1 Stratagene lung (#937210) Homo sapie | N | N | | N |

Table 2, cont.

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS33520 | D_RC_T67986_s | yc28e12.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82030 3' similar to | | | | |
| EOS30587 | B_RC_T94452 | ye36g7.s1 Stratagene lung (#93721) Homo sapiens | N | N | N | |
| EOS24288 | D_RC_N22495 | yw35g11.s1 Morton Fetal Cochlea Homo sapiens c | N | N | N | |
| EOS01767 | 1_M92843 | zinc finger protein homologous to Zfp-36 in mouse | N | N | N | |
| EOS26329 | N_312729_1 | zl16d08.r1 Soares_pregnant_uterus_NbHPU Homo | N | N | N | |
| EOS33680 | 1_X95735 D_RC_H | zyxin | Y | N | N | |
| EOS29695 | M86933 | amelogenin (Y chromosome) | Y | N | N | |
| EOS27689 | AI369384 | arylsulfatase D | N | N | N | |
| EOS31416 | X83107 | BMX non-receptor tyrosine kinase | N | N | N | |
| EOS32863 | AA598702 | bone morphogenetic protein 6 | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS03210 | X79981 | cadherin 5; VE-cadherin (vascular epithelium) | Y | Y | Type IIIb (Ne | YType IIIb (Nexo Ccyt) |
| EOS01275 | L76380 | calcitonin receptor-like | Y | Y | Type IIIa (clv | YType IIIa (clv) |
| EOS33843 | W84712 | calumenin | Y | N | N | |
| EOS03484 | Z18951 | caveolin 1; caveolae protein; 22kD | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS01027 | L06797 | chemokine (C-X-C motif); receptor 4 (fusin) | N | Y | Type IIIb (Ne | YType IIIb (Nexo Ccyt) |
| EOS35279 | D83174 | collagen-binding protein 2 (colligen 2) | Y | Y | Type Ia | YType Ia |
| EOS01768 | M92934 | connective tissue growth factor | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS00411 | HG1098-HT1098 | Cystatin D | | | | |
| EOS02094 | U18300 | damage-specific DNA binding protein 2 (48kD) | N | N | N | |
| EOS01954 | U03877 | EGF-containing fibulin-like extracellular matrix protei | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS01191 | L35545 | endothelial cell protein C/activated protein C recepto | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS31010 | J05008 | endothelin 1 | Y | N | N | |
| EOS17927 | N52090 | EST | | | | |
| EOS21265 | AA404418 | EST | | | | |
| EOS23893 | C13961 | EST | | | | |
| EOS04395 | N24990 | ESTs | N | N | N | |
| EOS04694 | AA025351 | ESTs | N | N | N | |
| EOS04716 | AA027168 | ESTs | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS04780 | AA040465 | ESTs | N | N | N | |
| EOS04795 | AA045136 | ESTs | N | N | N | |
| EOS05108 | AA187490 | ESTs | N | N | N | |
| EOS05193 | AA227926 | ESTs | N | N | N | |
| EOS05260 | AA234743 | ESTs | N | N | N | |
| EOS05659 | AA292694 | ESTs | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS05907 | AA406363 | ESTs | N | N | N | |

**Table 2, cont.**

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| EOS05938 | AA411465 | ESTs | N | N | N | | |
| EOS06054 | AA423987 | ESTs | N | N | N | | |
| EOS06085 | AA425309 | ESTs | N | N | Y | | |
| EOS06232 | AA435896 | ESTs | N | N | N | | |
| EOS06723 | AA478778 | ESTs | N | N | N | | |
| EOS07104 | AA621714 | ESTs | N | N | N | | |
| EOS08686 | AA127221 | ESTs | N | N | N | | |
| EOS08931 | AA156125 | ESTs | N | N | N | | |
| EOS09386 | AA232645 | ESTs | N | N | N | | |
| EOS09698 | F10399 | ESTs | N | Y | N | Type II (Ncyt Cexo) | Y |
| EOS10037 | H16772 | ESTs | N | N | N | | |
| EOS10836 | N39584 | ESTs | N | N | N | | |
| EOS11063 | N64436 | ESTs | N | N | Y | | |
| EOS11690 | R26892 | ESTs | N | N | N | | |
| EOS13003 | T33637 | ESTs | N | N | N | | |
| EOS14991 | AA253217 | ESTs | N | N | N | | |
| EOS15026 | AA255991 | ESTs | N | N | N | | |
| EOS15075 | AA258138 | ESTs | N | N | N | | |
| EOS15749 | AA426573 | ESTs | N | Y | N | Type II (Ncyt Cexo) | Y |
| EOS15877 | AA443793 | ESTs | N | N | N | | |
| EOS16244 | AA490588 | ESTs | N | N | N | | |
| EOS16519 | D59570 | ESTs | N | Y | Y | Type II (Ncyt Cexo) | Y |
| EOS16663 | F13787 | ESTs | N | N | N | | |
| EOS16953 | H88157 | ESTs | N | Y | N | Type II (Ncyt Cexo) | Y |
| EOS17116 | H98988 | ESTs | N | N | N | | |
| EOS19003 | R32894 | ESTs | N | N | N | | |
| EOS19085 | R61715 | ESTs | N | N | N | | |
| EOS23453 | AA608588 | ESTs | N | N | N | | |
| EOS23936 | D60302 | ESTs | N | N | N | | |
| EOS24599 | N95477 | ESTs | N | N | N | | |
| EOS26579 | AA856990 | ESTs | N | N | N | | |
| EOS26802 | AA136653 | ESTs | N | N | N | | |
| EOS27581 | AI123978 | ESTs | N | N | N | | |
| EOS27992 | AA379500 | ESTs | N | N | N | | |
| EOS28922 | R49693 | ESTs | N | N | N | | |

Table 2, cont.

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS29244 | AA028131 | ESTs | N | N | | N |
| EOS30569 | D59711 | ESTs | Y | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS30758 | AA053400 | ESTs | N | N | | N |
| EOS31112 | AA256153 | ESTs | N | N | | N |
| EOS31503 | AA046593 | ESTs | N | N | | N |
| EOS31577 | AA410480 | ESTs | N | Y | Type Ib (Nex | YType Ib (Nexo Ccyt) |
| EOS31686 | D45304 | ESTs | N | N | | N |
| EOS31980 | AA136353 | ESTs | N | N | | N |
| EOS32924 | AA505133 | ESTs | N | N | | N |
| EOS33091 | AA253193 | ESTs | Y | N | | N |
| EOS33130 | AA432248 | ESTs | N | N | | N |
| EOS33293 | AA479713 | ESTs | N | N | | N |
| EOS34229 | AA487558 | ESTs | N | N | | N |
| EOS34981 | C15324 | ESTs | | | | |
| EOS35003 | AA452000 | ESTs | N | N | | N |
| EOS14451 | AA046808 | ESTs; Highly similar to 40S RIBOSOMAL PROTEIN | N | N | | N |
| EOS25285 | R45630 | ESTs; Highly similar to KIAA0372 [H.sapiens] | N | N | | N |
| EOS27332 | AA358869 | ESTs; Highly similar to SEC13-RELATED PROTEIN | N | N | | N |
| EOS19796 | W80814 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | N | N | | N |
| EOS04882 | AA071089 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | Y | N | | N |
| EOS23463 | AA608751 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] | | | | |
| EOS23090 | AA488687 | ESTs; Moderately similar to !!!! ALU SUBFAMILY S | Y | N | | N |
| EOS23403 | AA599143 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | | | | |
| EOS05756 | AA398243 | ESTs; Moderately similar to (defline not available 36 | N | N | | N |
| EOS08776 | AA132983 | ESTs; Moderately similar to C-1-TETRAHYDROFOL | N | N | | N |
| EOS25520 | R23858 | ESTs; Moderately similar to envelope protein [H.sap | Y | N | | N |
| EOS13853 | W80763 | ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus] | | | | |
| EOS21311 | AA405747 | ESTs; Moderately similar to HMG-box transcription f | N | N | | N |
| EOS32690 | H99198 | ESTs; Moderately similar to THYMOSIN BETA-4 [H. | N | N | | N |
| EOS24805 | R70506 | ESTs; Moderately similar to transformation-related p | N | N | | N |
| EOS34919 | AA236324 | ESTs; Weakly similar to !!!! ALU CLASS A WARNIN | Y | N | | N |
| EOS18405 | N66845 | ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens] | | | | |
| EOS24777 | R60044 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WA | N | N | | N |
| EOS32606 | AA283035 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WA | Y | N | | N |
| EOS08818 | AA135606 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens] | | | | |

**Table 2, cont.**

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS16269 | AA496257 | ESTs; Weakly similar to (defline not available 35133 | N | | N | |
| EOS28441 | AI024874 | ESTs; Weakly similar to (defline not available 38822 | N | | N | |
| EOS16360 | AA609717 | ESTs; Weakly similar to MICROTUBULE-ASSOCIA | N | | N | |
| EOS05306 | AA236559 | ESTs; Weakly similar to neuronal thread protein AD | Y | Type II (Ncyt | Y | Type II (Ncyt Cexo) |
| EOS25033 | T95333 | ESTs; Weakly similar to Strabismus [D.melanogaste | N | | N | |
| EOS01787 | M94856 | fatty acid binding protein 5 (psoriasis-associated) | N | | N | |
| EOS33537 | M34539 | FK506-binding protein 1A (12kD) | N | | N | |
| EOS33447 | X52947 | gap junction protein; alpha 1; 43kD (connexin 43) | N | Type IIIa (Nc | Y | Type IIIa (Ncyt Cexo) |
| EOS33557 | U09587 | glycyl-tRNA synthetase | Y | | N | |
| EOS02213 | U31384 | guanine nucleotide binding protein 11 | N | | N | |
| EOS00414 | HG1103-HT1103 | Guanine Nucleotide-Binding Protein Rai, Ras-Oncogene Related | | | | |
| EOS04904 | AA085918 | H.sapiens HUNKI mRNA | N | | N | |
| EOS03115 | X69910 | H.sapiens p63 mRNA for transmembrane protein | N | | N | |
| EOS32288 | X60486 | H4 histone family; member G | N | | N | |
| EOS03088 | X67235 | hematopoietically expressed homeobox | Y | | N | |
| EOS10936 | N53375 | Homer; neuronal immediate early gene; 3 | N | | N | |
| EOS33421 | L40395 | Homo sapiens clone 23689 mRNA; complete cds | N | | N | |
| EOS28978 | AA195678 | Homo sapiens mRNA for KIAA0465 protein; partial c | N | | N | |
| EOS32898 | N77151 | Homo sapiens mRNA for KIAA0799 protein; partial c | N | | N | |
| EOS06353 | AA448238 | Homo sapiens mRNA for KIAA0915 protein; complet | N | | N | |
| EOS00335 | D86425 | Homo sapiens mRNA for nidogen-2 | Y | | N | |
| EOS10948 | N54067 | Homo sapiens mRNA for NIK; partial cds | | | | |
| EOS30902 | AA370302 | Homo sapiens mRNA; cDNA DKFZp586I1518 (from | Y | | N | |
| EOS04522 | R81003 | Homo sapiens serine protease mRNA; complete cds | Y | | N | |
| EOS01377 | M21305 | Human alpha satellite and satellite 3 junction DNA sequence | | | | |
| EOS01098 | L15388 | Human G protein-coupled receptor kinase (GRK5) | N | | N | |
| EOS33621 | M85289 | Human heparan sulfate proteoglycan (HSPG2) mRN | Y | | N | |
| EOS07146 | D51069 | Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds | | | | |
| EOS34018 | D43636 | Human mRNA for KIAA0096 gene; partial cds | N | | N | |
| EOS00350 | D86983 | Human mRNA for KIAA0230 gene; partial cds | Y | | N | |
| EOS32617 | AB002301 | Human mRNA for KIAA0303 gene; partial cds | N | | N | |
| EOS02817 | X04729 | Human mRNA for plasminogen activator inhibitor typ | N | | N | |
| EOS34346 | M28882 | Human MUC18 glycoprotein mRNA, complete cds | Y | Type Ia | Y | Type Ia |
| EOS01644 | M68874 | Human phosphatidylcholine 2-acylhydrolase (cPLA2 | N | | N | |
| EOS02171 | U27109 | Human prepromultimerin mRNA; complete cds | Y | | N | |

**Table 2, cont.**

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| EOS29301 | M10321 | Human von Willebrand factor mRNA, 3' end | Y | N | | N | |
| EOS00648 | HG3342-HT3519 | Id1 | | | | | |
| EOS34091 | U97188 | IGF-II mRNA-binding protein 3 | N | N | | N | |
| EOS02828 | X06256 | integrin; alpha 5 (fibronectin receptor; alpha polypep | N | N | | N | |
| EOS01490 | M32334 | intercellular adhesion molecule 2 | Y | Y | Type Ia | N | YType Ia |
| EOS33077 | D12763 | interleukin 1 receptor-like 1 | Y | N | | N | |
| EOS02593 | U70322 | karyopherin (importin) beta 2 | N | N | | N | |
| EOS32386 | AA114250 | KIAA0512 gene product | Y | N | | N | |
| EOS02689 | U81607 | kinase scaffold protein gravin | N | N | | N | |
| EOS33969 | S78569 | laminin; alpha 4 | Y | N | | N | |
| EOS01604 | M61916 | laminin; beta 1 | Y | N | | N | |
| EOS32420 | F13782 | LIM binding domain 2 | N | N | | N | |
| EOS29814 | AA286710 | lymphocyte adaptor protein | N | N | | N | |
| EOS02734 | U89942 | lysyl oxidase-like 2 | Y | N | | N | |
| EOS02494 | U59423 | MAD (mothers against decapentaplegic; Drosophila) | N | N | | N | |
| EOS32666 | U68019 | MAD (mothers against decapentaplegic; Drosophila) | N | N | | N | |
| EOS02966 | X54925 | matrix metalloproteinase 1 (interstitial collagenase) | Y | N | | N | |
| EOS02845 | X07820 | matrix metalloproteinase 10 (stromelysin 2) | Y | N | | N | |
| EOS32343 | AA132969 | metalloprotease 1 (pitrilysin family) | N | N | | N | |
| EOS33626 | D10522 | myristoylated alanine-rich protein kinase C substrate | N | N | | N | |
| EOS31067 | U85193 | nuclear factor I/B | N | N | | N | |
| EOS01473 | M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | Y | N | | N | |
| EOS01124 | L20971 | phosphodiesterase 4B; cAMP-specific (dunce (Dros | N | Y | Type Ib (Nex | Y | YType Ib (Nexo Ccyt) |
| EOS04824 | AA054087 | phospholipase A2; group IVC (cytosolic; calcium-ind | N | Y | Type Ib (Nex | Y | YType Ib (Nexo Ccyt) |
| EOS32013 | Y07867 | pirin | N | N | | N | |
| EOS02967 | X54936 | placental growth factor; vascular endothelial growth f | Y | N | | N | |
| EOS00921 | J03764 | plasminogen activator inhibitor; type I | N | N | | N | |
| EOS01480 | M31551 | plasminogen activator inhibitor; type II (arginine-serp | N | N | | N | |
| EOS33915 | L34657 | platelet/endothelial cell adhesion molecule (CD31 an | Y | Y | Type Ia | Y | YType Ia |
| EOS07315 | U97519 | podocalyxin-like | N | Y | Type IIIa (Nc | Y | YType IIIa (Ncyt Cexo) |
| EOS05961 | AA412284 | poliovirus receptor | Y | N | | N | |
| EOS32094 | U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (ly | N | N | | N | |
| EOS03096 | X67951 | proliferation-associated gene A (natural killer-enhan | N | N | | N | |
| EOS32991 | AB000584 | prostate differentiation factor | Y | N | | N | |
| EOS02233 | U33053 | protein kinase C-like 1 | N | N | | N | |

**Table 2, cont.**

| | | | | | | |
|---|---|---|---|---|---|---|
| EOS09096 | AA179845 | RAB6 interacting; kinesin-like (rabkinesin6) | N | N | | N |
| EOS30425 | AA243278 | ribosomal protein; mitochondrial; L12 | N | N | | N |
| EOS33544 | D67029 | SEC14 (S. cerevisiae)-like | N | N | | N |
| EOS29398 | J03040 | secreted protein; acidic; cysteine-rich (osteonectin) | Y | N | | N |
| EOS01415 | M24736 | selectin E (endothelial adhesion molecule 1) | Y | Y | Type Ia | YType Ia |
| EOS01942 | U03057 | singed (Drosophila)-like (sea urchin fascin homolog l | N | N | | N |
| EOS32648 | AA056731 | Sjogren syndrome antigen A2 (60kD; ribonucleoprot | N | N | | N |
| EOS18509 | N68905 | small inducible cytokine A5 (RANTES) | | | | |
| EOS19346 | T97186 | small inducible cytokine A5 (RANTES) | | | | |
| EOS34383 | X70683 | SRY (sex determining region Y)-box 4 | N | N | | N |
| EOS02708 | U83463 | syndecan binding protein (syntenin) | N | N | | N |
| EOS34586 | X14787 | thrombospondin 1 | Y | N | | N |
| EOS33905 | D29992 | tissue factor pathway inhibitor 2 | Y | N | | N |
| EOS01671 | M74719 | transcription factor 4 | N | N | | N |
| EOS24589 | N93521 | transcription factor 4 | N | N | | N |
| EOS31789 | M90657 | transmembrane 4 superfamily member 1 | Y | Y | Type IIIa (clv | YType IIIa (clv) |
| EOS29735 | AA012933 | tubulin-specific chaperone d | N | N | | N |
| EOS03025 | X60957 | tyrosine kinase with immunoglobulin and epidermal | Y | N | | N |
| EOS26493 | W26247 | U5 snRNP-specific protein (220 kD); ortholog of S. c | N | N | | N |
| EOS07225 | T34527 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N | Y | N | | N |
| EOS10914 | N52006 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N | N | N | | N |
| EOS17493 | N34287 | unc5 (C.elegans homolog) C | Y | Y | Type Ia | YType Ia |
| EOS31811 | AA010163 | upstream regulatory element binding protein 1 | N | N | | N |
| EOS29118 | M30257 | vascular cell adhesion molecule 1 | Y | Y | Type IIIa (Nc | YType IIIa (Ncyt Cexo) |
| EOS33480 | W80846 | vesicle-associated membrane protein 5 (myobrevin) | N | Y | Type II (Ncyt | YType II (Ncyt Cexo) |
| EOS24245 | H94892 | v-ral simian leukemia viral oncogene homolog A (ras | N | N | | N |
| EOS33190 | AA083572 | v-ral simian leukemia viral oncogene homolog A (ras | N | N | | N |
| EOS13125 | T57112 | yc20g11.s1 Stratagene lung (#937210) Homo sapie | N | N | | N |
| EOS25020 | T91518 | ye20f05.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118305 3' similar t | | | | |
| EOS30587 | T94452 | ye36g7.s1 Stratagene lung (#93721) Homo sapiens | N | N | | N |
| EOS25495 | R20839 | yg05c07.r1 Soares infant brain 1NIB Homo sapiens | N | N | | N |
| EOS19104 | R71234 | yi54c08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143054 3' similar to g | | | | |
| EOS19151 | R98105 | yr30g11.s1 Soares fetal liver spleen 1NFLS Homo s | N | N | | N |
| EOS03780 | AA187101 | zp61b8.r1 Stratagene endothelial cell 937223 Homo | N | N | | N |

TABLE 3

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| D86425 | Homo sapiens mRNA for nidogen-2 | Hs.82733 |
| D86983 | Human mRNA for KIAA0230 gene; partial cds | Hs.118893 |
| HG1098-HT1098 | Cystatin D | |
| HG1103-HT1103 | "Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene | |
| HG3342-HT3519 | Id1 | |
| J03764 | plasminogen activator inhibitor; type I | Hs.82085 |
| L06797 | chemokine (C-X-C motif); receptor 4 (fusin) | Hs.89414 |
| L15388 | "Human G protein-coupled receptor kinase (GRK5) mRNA, | Hs.211569 |
| L20971 | phosphodiesterase 4B; cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) | Hs.188 |
| L35545 | endothelial cell protein C/activated protein C receptor | Hs.82353 |
| L76380 | calcitonin receptor-like | Hs.152175 |
| M21305 | Human alpha satellite and satellite 3 junction DNA sequence | Hs.247946 |
| M24736 | selectin E (endothelial adhesion molecule 1) | Hs.89546 |
| M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | Hs.2050 |
| M31551 | plasminogen activator inhibitor; type II (arginine-serpin) | Hs.75716 |
| M32334 | intercellular adhesion molecule 2 | Hs.83733 |
| M61916 | laminin; beta 1 | Hs.82124 |
| M68874 | "Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, | |
| M74719 | transcription factor 4 | Hs.75356 |
| M92934 | connective tissue growth factor | Hs.75511 |
| M94856 | fatty acid binding protein 5 (psoriasis-associated) | Hs.153179 |
| U03057 | singed (Drosophila)-like (sea urchin fascin homolog like) | Hs.118400 |
| U03877 | EGF-containing fibulin-like extracellular matrix protein 1 | Hs.76224 |
| U18300 | damage-specific DNA binding protein 2 (48kD) | Hs.77602 |
| U27109 | Human prepromultimerin mRNA; complete cds | Hs.32934 |
| U31384 | guanine nucleotide binding protein 11 | Hs.83381 |
| U33053 | protein kinase C-like 1 | Hs.2499 |
| U59423 | MAD (mothers against decapentaplegic; Drosophila) homolog 1 | Hs.79067 |
| U70322 | karyopherin (importin) beta 2 | Hs.168075 |
| U81607 | kinase scaffold protein gravin | Hs.788 |
| U83463 | syndecan binding protein (syntenin) | Hs.8180 |
| U89942 | lysyl oxidase-like 2 | Hs.83354 |
| X04729 | Human mRNA for plasminogen activator inhibitor type 1 | |
| X06256 | integrin; alpha 5 (fibronectin receptor; alpha polypeptide) | Hs.149609 |
| X07820 | matrix metalloproteinase 10 (stromelysin 2) | Hs.2258 |
| X54925 | matrix metalloproteinase 1 (interstitial collagenase) | Hs.83169 |
| X54936 | placental growth factor; vascular endothelial growth factor-related | Hs.2894 |
| X60957 | tyrosine kinase with immunoglobulin and epidermal growth factor | Hs.78824 |
| X67235 | hematopoietically expressed homeobox | Hs.118651 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| X67951 | proliferation-associated gene A (natural killer-enhancing factor A) | Hs.180909 |
| X69910 | H.sapiens p63 mRNA for transmembrane protein | Hs.74368 |
| X79981 | cadherin 5; VE-cadherin (vascular epithelium) | Hs.76206 |
| Z18951 | caveolin 1; caveolae protein; 22kD | Hs.247266 |
| AA187101 | "zp61b6.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:624659 5', mRNA sequence" | |
| N24990 | ESTs | Hs.26418 |
| R81003 | Homo sapiens serine protease mRNA; complete cds | Hs.154737 |
| AA025351 | ESTs | Hs.134797 |
| AA027168 | ESTs | Hs.10031 |
| AA040465 | ESTs | Hs.8728 |
| AA045136 | ESTs | Hs.22575 |
| AA054087 | phospholipase A2; group IVC (cytosolic; calcium-independent) | Hs.18858 |
| AA071089 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING | Hs.187932 |
| AA085918 | H.sapiens HUNKI mRNA | Hs.247482 |
| AA187490 | ESTs | Hs.21941 |
| AA227926 | ESTs | Hs.6682 |
| AA234743 | ESTs | Hs.22120 |
| AA236559 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP | Hs.8768 |
| AA292694 | ESTs | Hs.3807 |
| AA398243 | ESTs; Moderately similar to (defline not available 3694664) | Hs.21806 |
| AA406363 | ESTs | Hs.30822 |
| AA411465 | ESTs | Hs.8619 |
| AA412284 | poliovirus receptor | Hs.171844 |
| AA423987 | ESTs | Hs.7567 |
| AA425309 | ESTs | Hs.33287 |
| AA435896 | ESTs | Hs.18397 |
| AA448238 | Homo sapiens mRNA for KIAA0915 protein; complete cds | Hs.16714 |
| AA478778 | ESTs | Hs.16450 |
| AA621714 | ESTs | Hs.25338 |
| D51069 | Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); | Hs.211579 |
| T34527 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | Hs.80120 |
| U97519 | podocalyxin-like | Hs.16426 |
| AA127221 | ESTs | Hs.71059 |
| AA132983 | ESTs; Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE; CYTOPLASMIC [H.sapiens] | Hs.44155 |
| AA135606 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING | Hs.189384 |
| AA156125 | ESTs | Hs.72116 |
| AA179845 | RAB6 interacting; kinesin-like (rabkinesin6) | Hs.73625 |
| AA232645 | ESTs | Hs.42699 |
| F10399 | ESTs | Hs.14763 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| H16772 | ESTs | Hs.31444 |
| N39584 | ESTs | Hs.17404 |
| N52006 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | Hs.80120 |
| N53375 | Homer; neuronal immediate early gene; 3 | Hs.166146 |
| N54067 | Homo sapiens mRNA for NIK; partial cds | Hs.3628 |
| N64436 | ESTs | Hs.20813 |
| R26892 | ESTs | Hs.221434 |
| T33637 | ESTs | Hs.6841 |
| T57112 | "yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence." | |
| W80763 | ESTs; Moderately similar to FK506-binding protein 65kD | Hs.3849 |
| AA046808 | ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S27 | Hs.108957 |
| AA253217 | ESTs | Hs.41271 |
| AA255991 | ESTs | Hs.175319 |
| AA258138 | ESTs | Hs.88297 |
| AA426573 | ESTs | Hs.41135 |
| AA443793 | ESTs | Hs.94761 |
| AA490588 | ESTs | Hs.43118 |
| AA496257 | ESTs; Weakly similar to (defline not available 3513303) | Hs.72165 |
| AA609717 | ESTs; Weakly similar to MICROTUBULE-ASSOCIATED | Hs.66048 |
| D59570 | ESTs | Hs.17132 |
| F13787 | ESTs | Hs.58596 |
| H88157 | ESTs | Hs.41105 |
| H98988 | ESTs | Hs.42612 |
| N34287 | unc5 (C.elegans homolog) C | Hs.44553 |
| N52090 | EST | Hs.47420 |
| N66845 | ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! | Hs.165411 |
| N68905 | small inducible cytokine A5 (RANTES) | |
| R32894 | ESTs | Hs.45514 |
| R61715 | ESTs | Hs.138237 |
| R71234 | "yi54c08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143054 3' similar to gb\|M87908\|HUMALNE32 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:S41458 ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE | |
| R98105 | "yr30g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206852 3', mRNA sequence." | |
| T97186 | small inducible cytokine A5 (RANTES) | |
| W80814 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING | Hs.193700 |
| AA404418 | EST | Hs.144953 |
| AA405747 | ESTs; Moderately similar to HMG-box transcription factor | Hs.97865 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA488687 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING | Hs.190307 |
| AA599143 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING | |
| AA608588 | ESTs | Hs.193634 |
| AA608751 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING | Hs.244904 |
| C13961 | EST | Hs.210115 |
| D60302 | ESTs | Hs.108977 |
| H94892 | v-ral simian leukemia viral oncogene homolog A (ras related) | Hs.6906 |
| N93521 | transcription factor 4 | Hs.241362 |
| N95477 | ESTs | Hs.102943 |
| R60044 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | Hs.106706 |
| R70506 | ESTs; Moderately similar to transformation-related protein | Hs.107159 |
| T91518 | "ye20f05.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118305 3' similar to contains Alu repetitive element;contains MER12 repetitive element ;, mRNA sequence." | |
| T95333 | ESTs; Weakly similar to Strabismus [D.melanogaster] | Hs.122730 |
| R45630 | ESTs; Highly similar to KIAA0372 [H.sapiens] | Hs.170098 |
| R20839 | "yg05c07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31444 5', mRNA sequence." | |
| R23858 | ESTs; Moderately similar to envelope protein [H.sapiens] | Hs.23986 |
| AI024874 | ESTs; Weakly similar to (defline not available 3882257) | Hs.57958 |
| W26247 | U5 snRNP-specific protein (220 kD); ortholog of S. cerevisiae | Hs.6413 |
| AA856990 | ESTs | Hs.125058 |
| AA136653 | ESTs | |
| AA358869 | ESTs; Highly similar to SEC13-RELATED PROTEIN [H.sapiens] | Hs.227949 |
| AI123976 | ESTs | Hs.105689 |
| AI369384 | arylsulfatase D | |
| AA379500 | ESTs | Hs.193155 |
| R49693 | ESTs | Hs.107708 |
| AA195678 | Homo sapiens mRNA for KIAA0465 protein; partial cds | Hs.108258 |
| M30257 | vascular cell adhesion molecule 1 | Hs.109225 |
| AA028131 | ESTs | Hs.110342 |
| M10321 | "Human von Willebrand factor mRNA, 3' end" | Hs.110802 |
| J03040 | secreted protein; acidic; cysteine-rich (osteonectin) | Hs.111779 |
| M86933 | amelogenin (Y chromosome) | Hs.1238 |
| AA012933 | tubulin-specific chaperone d | Hs.241687 |
| AA286710 | lymphocyte adaptor protein | Hs.13131 |
| AA243278 | ribosomal protein; mitochondrial; L12 | Hs.109059 |
| D59711 | ESTs | Hs.237289 |
| T94452 | "ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence" | Hs.241207 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA053400 | ESTs | Hs.241227 |
| AA370302 | Homo sapiens mRNA; cDNA DKFZp586I1518 (from clone | Hs.21739 |
| J05008 | endothelin 1 | Hs.2271 |
| U85193 | nuclear factor I/B | Hs.33287 |
| AA256153 | ESTs | Hs.23912 |
| X83107 | BMX non-receptor tyrosine kinase | Hs.27372 |
| AA046593 | ESTs | Hs.28959 |
| AA410480 | ESTs | Hs.30089 |
| D45304 | ESTs | Hs.31595 |
| M90657 | transmembrane 4 superfamily member 1 | Hs.3337 |
| AA010163 | upstream regulatory element binding protein 1 | Hs.3383 |
| AA136353 | ESTs | Hs.38022 |
| Y07867 | pirin | Hs.38842 |
| U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine | Hs.41270 |
| X60486 | H4 histone family; member G | Hs.46423 |
| AA132969 | metalloprotease 1 (pitrilysin family) | Hs.4812 |
| AA114250 | KIAA0512 gene product | Hs.48924 |
| F13782 | LIM binding domain 2 | Hs.4980 |
| AA283035 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | Hs.54813 |
| AB002301 | Human mRNA for KIAA0303 gene; partial cds | Hs.54985 |
| AA056731 | Sjogren syndrome antigen A2 (60kD; ribonucleoprotein | Hs.554 |
| U68019 | MAD (mothers against decapentaplegic; Drosophila) homolog 3 | Hs.211578 |
| H99198 | ESTs; Moderately similar to THYMOSIN BETA-4 [H.sapiens] | Hs.56145 |
| AA598702 | bone morphogenetic protein 6 | Hs.6101 |
| N77151 | Homo sapiens mRNA for KIAA0799 protein; partial cds | Hs.61638 |
| AA505133 | ESTs | Hs.62273 |
| AB000584 | prostate differentiation factor | Hs.116577 |
| D12763 | interleukin 1 receptor-like 1 | Hs.66 |
| AA253193 | ESTs | Hs.6631 |
| AA432248 | ESTs | Hs.6738 |
| AA083572 | v-ral simian leukemia viral oncogene homolog A (ras related) | Hs.6906 |
| AA479713 | ESTs | Hs.71962 |
| L40395 | Homo sapiens clone 23689 mRNA; complete cds | Hs.170001 |
| X52947 | gap junction protein; alpha 1; 43kD (connexin 43) | Hs.74471 |
| W80846 | vesicle-associated membrane protein 5 (myobrevin) | Hs.74669 |
| M34539 | FK506-binding protein 1A (12kD) | Hs.752 |
| D67029 | SEC14 (S. cerevisiae)-like | Hs.75232 |
| U09587 | glycyl-tRNA synthetase | Hs.75280 |
| M85289 | "Human heparan sulfate proteoglycan (HSPG2) mRNA, complete | Hs.211573 |
| D10522 | myristoylated alanine-rich protein kinase C substrate (MARCKS; | Hs.75607 |
| W84712 | calumenin | Hs.7753 |
| D29992 | tissue factor pathway inhibitor 2 | Hs.78045 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| L34657 | platelet/endothelial cell adhesion molecule (CD31 antigen) | Hs.78146 |
| S78569 | laminin; alpha 4 | Hs.78672 |
| D43636 | Human mRNA for KIAA0096 gene; partial cds | Hs.79025 |
| U97188 | IGF-II mRNA-binding protein 3 | Hs.79440 |
| AA487558 | ESTs | Hs.8135 |
| M28882 | "Human MUC18 glycoprotein mRNA, complete cds" | Hs.211579 |
| X70683 | SRY (sex determining region Y)-box 4 | Hs.83484 |
| X14787 | thrombospondin 1 | Hs.87409 |
| AA236324 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! | Hs.92381 |
| C15324 | ESTs | Hs.93668 |
| AA452000 | ESTs | Hs.94030 |
| D83174 | collagen-binding protein 2 (colligen 2) | Hs.9930 |
| D00596 | Homo sapiens gene for thymidylate synthase; exons 1; 2; 3; 4; 5; | Hs.196351 |
| D11428 | peripheral myelin protein 22 | Hs.103724 |
| D13640 | major histocompatibility complex; class I; C | Hs.183618 |
| D14874 | adrenomedullin | Hs.394 |
| D26129 | ribonuclease; RNase A family; 1 (pancreatic) | Hs.78224 |
| D28476 | thyroid hormone receptor interactor 12 | Hs.138617 |
| D86425 | Homo sapiens mRNA for nidogen-2 | Hs.82733 |
| D86983 | Human mRNA for KIAA0230 gene; partial cds | Hs.118893 |
| D87953 | N-myc downstream regulated | Hs.75789 |
| HG1862-HT1897 | Calmodulin Type I | |
| HG2614-HT2710 | "Collagen, Type Viii, Alpha 1" | |
| HG2639-HT2735 | Single-Stranded Dna-Binding Protein Mssp-1 | |
| HG2855-HT2995 | "Heat Shock Protein, 70 Kda (Gb:Y00371)" | |
| HG3044-HT3742 | "Fibronectin, Alt. Splice 1" | |
| HG3342-HT3519 | Id1 | |
| HG3543-HT3739 | Insulin-Like Growth Factor 2 | |
| HG4069-HT4339 | Monocyte Chemotactic Protein 1 | |
| HG417-HT417 | Cathepsin B | |
| J03764 | plasminogen activator inhibitor; type I | Hs.82085 |
| L06797 | chemokine (C-X-C motif); receptor 4 (fusin) | Hs.89414 |
| L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | Hs.86386 |
| L12711 | transketolase (Wernicke-Korsakoff syndrome) | Hs.89643 |
| L13977 | prolylcarboxypeptidase (angiotensinase C) | Hs.75693 |
| L15388 | "Human G protein-coupled receptor kinase (GRK5) mRNA, | |
| L19871 | activating transcription factor 3 | Hs.460 |
| L20859 | Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds | Hs.78452 |
| L42176 | four and a half LIM domains 2 | Hs.8302 |
| L49169 | Human G0S3 mRNA; complete cds | Hs.75678 |
| L76380 | calcitonin receptor-like | Hs.152175 |
| M15990 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 | Hs.194148 |
| M23254 | calpain; large polypeptide L2 | Hs.76288 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| M24736 | selectin E (endothelial adhesion molecule 1) | Hs.89546 |
| M26576 | collagen; type IV; alpha 1 | Hs.119129 |
| M27396 | asparagine synthetase | Hs.75692 |
| M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | Hs.2050 |
| M31994 | "Homo sapiens aldehyde dehydrogenase (ALDH1) gene, exon 13 | |
| M32334 | intercellular adhesion molecule 2 | Hs.83733 |
| M35878 | insulin-like growth factor binding protein 3 | Hs.77326 |
| M36429 | postmeiotic segregation increased 2-like 12 | Hs.89672 |
| M57730 | ephrin-A1 | Hs.1624 |
| M57731 | GRO2 oncogene | Hs.75765 |
| M60858 | nucleolin | Hs.79110 |
| M62994 | filamin B; beta (actin-binding protein-278) | Hs.81008 |
| M68874 | "Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, | |
| M69043 | nuclear factor of kappa light polypeptide gene enhancer in B-cells | Hs.81328 |
| M74719 | transcription factor 4 | Hs.75356 |
| M75126 | hexokinase 1 | Hs.118625 |
| M84349 | CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5; EJ16; EJ30; EL32 and G344) | Hs.119663 |
| M92843 | zinc finger protein homologous to Zfp-36 in mouse | Hs.198309 |
| M92934 | connective tissue growth factor | Hs.75511 |
| M93056 | protease inhibitor 2 (anti-elastase); monocyte/neutrophil | Hs.183583 |
| M94856 | fatty acid binding protein 5 (psoriasis-associated) | Hs.153179 |
| M95787 | transgelin | Hs.75777 |
| S76965 | Protein kinase inhibitor [human; neuroblastoma cell line | Hs.75209 |
| S81914 | DIFFERENTIATION-DEPENDENT GENE 2 | Hs.76095 |
| U03057 | singed (Drosophila)-like (sea urchin fascin homolog like) | Hs.118400 |
| U03100 | catenin (cadherin-associated protein); alpha 1 (102kD) | Hs.178452 |
| U03877 | EGF-containing fibulin-like extracellular matrix protein 1 | Hs.76224 |
| U08021 | nicotinamide N-methyltransferase | Hs.76669 |
| U14391 | myosin IC | Hs.82251 |
| U31384 | guanine nucleotide binding protein 11 | Hs.83381 |
| U32944 | dynein; cytoplasmic; light polypeptide | Hs.5120 |
| U40369 | "Human spermidine/spermine N1-acetyltransferase (SSAT) gene, | |
| U41767 | "Human metargidin precursor mRNA, complete cds" | |
| U48959 | Homo sapiens myosin light chain kinase (MLCK) mRNA; | Hs.75950 |
| U51010 | "Human nicotinamide N-methyltransferase gene, exon 1 and 5' | |
| U51478 | ATPase; Na+/K+ transporting; beta 3 polypeptide | Hs.76941 |
| U53445 | Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA; complete cds | Hs.15432 |
| U59289 | cadherin 13; H-cadherin (heart) | Hs.63984 |
| U59423 | MAD (mothers against decapentaplegic; Drosophila) homolog 1 | Hs.79067 |
| U62015 | "Homo sapiens Cyr61 mRNA, complete cds" | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| U63825 | Human hepatitis delta antigen interacting protein A (dipA) mRNA; | Hs.66713 |
| U67963 | Human lysophospholipase homolog (HU-K5) mRNA; complete | Hs.6721 |
| U73379 | Human cyclin-selective ubiquitin carrier protein mRNA; complete | Hs.93002 |
| U73824 | eukaryotic translation initiation factor 4 gamma; 2 | Hs.183684 |
| U77604 | microsomal glutathione S-transferase 2 | Hs.81874 |
| U81607 | kinase scaffold protein gravin | Hs.788 |
| U89942 | lysyl oxidase-like 2 | Hs.83354 |
| X04412 | gelsolin (amyloidosis; Finnish type) | Hs.80562 |
| X06985 | heme oxygenase (decycling) 1 | Hs.75967 |
| X07820 | matrix metalloproteinase 10 (stromelysin 2) | Hs.2258 |
| X12876 | keratin 18 | Hs.65114 |
| X15729 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase; | Hs.76053 |
| X52541 | early growth response 1 | Hs.738 |
| X53416 | filamin A; alpha (actin-binding protein-280) | Hs.76279 |
| X54489 | GRO1 oncogene (melanoma growth stimulating activity; alpha) | Hs.789 |
| X54925 | matrix metalloproteinase 1 (interstitial collagenase) | Hs.83169 |
| X57206 | inositol 1;4;5-trisphosphate 3-kinase B | Hs.78877 |
| X59798 | cyclin D1 (PRAD1; parathyroid adenomatosis 1) | Hs.82932 |
| X60957 | tyrosine kinase with immunoglobulin and epidermal growth factor | Hs.78824 |
| X65965 | H.sapiens SOD-2 gene for manganese superoxide dismutase | |
| X69111 | inhibitor of DNA binding 3; dominant negative helix-loop-helix | Hs.76884 |
| X70940 | eukaryotic translation elongation factor 1 alpha 2 | Hs.2642 |
| X87838 | catenin (cadherin-associated protein); beta 1 (88kD) | Hs.171271 |
| X91247 | thioredoxin reductase 1 | Hs.13046 |
| X97748 | H.sapiens PTX3 gene promotor region | |
| Y00815 | protein tyrosine phosphatase; receptor type; F | Hs.75216 |
| AA303711 | ephrin-B1 | Hs.144700 |
| L44538 | ESTs | Hs.156044 |
| AA025351 | ESTs | Hs.134797 |
| AA027050 | ESTs | Hs.31189 |
| AA029462 | ESTs | Hs.17235 |
| AA045136 | ESTs | Hs.22575 |
| AA047437 | ESTs | Hs.22968 |
| AA054087 | phospholipase A2; group IVC (cytosolic; calcium-independent) | Hs.18858 |
| AA071089 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING | Hs.187932 |
| AA156450 | ESTs; Weakly similar to Similar to Rat trg gene product | Hs.8982 |
| AA187490 | ESTs | Hs.21941 |
| AA195031 | ESTs; Moderately similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [H.sapiens] | Hs.9305 |
| AA205724 | ESTs | Hs.10119 |
| AA227926 | ESTs | Hs.6682 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA227986 | ESTs | Hs.25329 |
| AA234743 | ESTs | Hs.22120 |
| AA253216 | ESTs | Hs.22283 |
| AA256210 | oncomodulin | Hs.199134 |
| AA256268 | ESTs | Hs.10283 |
| AA279397 | ESTs; Moderately similar to fibronectin [H.sapiens] | Hs.25001 |
| AA292379 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING | Hs.20340 |
| AA292717 | ESTs; Weakly similar to JM2 [H.sapiens] | Hs.7891 |
| AA346551 | ESTs | Hs.23457 |
| AA400292 | ESTs | Hs.23786 |
| AA404338 | ESTs | Hs.21812 |
| AA412284 | poliovirus receptor | Hs.171844 |
| AA423987 | ESTs | Hs.7567 |
| AA428594 | ESTs | Hs.21321 |
| AA430108 | ESTs | Hs.6019 |
| AA431462 | ESTs | Hs.28329 |
| AA431470 | ESTs; Weakly similar to CAMP-DEPENDENT PROTEIN KINASE INHIBITOR; MUSCLE/BRAIN FORM [H.sapiens] | Hs.3407 |
| AA443756 | ESTs; Moderately similar to (defline not available 4105275) | Hs.6673 |
| AA449479 | ESTs; Highly similar to (defline not available 5106787) | Hs.5216 |
| AA459916 | bradykinin receptor B2 | Hs.25021 |
| AA465226 | ESTs | Hs.28631 |
| AA478778 | ESTs | Hs.16450 |
| AA479037 | ESTs | Hs.7961 |
| AA482597 | ESTs; Highly similar to (defline not available 4704739) | Hs.26054 |
| AA487561 | ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1A | Hs.9813 |
| AA489245 | ESTs; Weakly similar to sperm specific protein [H.sapiens] | Hs.5682 |
| AA504110 | ESTs | Hs.18063 |
| AA520989 | ESTs; Highly similar to SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT [H.sapiens] | Hs.9195 |
| AA599434 | ESTs | Hs.25035 |
| AA608649 | Homo sapiens clone 23742 mRNA; partial cds | Hs.6354 |
| AA609519 | ESTs | Hs.26458 |
| D51069 | Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); | Hs.185718 |
| U97519 | podocalyxin-like | Hs.16426 |
| W28391 | proliferation-associated 2G4; 38kD | Hs.5181 |
| AA035638 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone | Hs.71968 |
| AA083514 | ESTs | Hs.68301 |
| AA121315 | ESTs | Hs.70823 |
| AA147186 | ESTs | Hs.92387 |
| AA156125 | ESTs | Hs.72116 |
| AA188932 | ESTs | Hs.85640 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA219653 | ESTs | Hs.87125 |
| AA232645 | ESTs | Hs.42699 |
| F10078 | ESTs | Hs.13233 |
| H48032 | ESTs | Hs.9645 |
| H82117 | ESTs | Hs.28043 |
| N39584 | ESTs | Hs.17404 |
| N54067 | Homo sapiens mRNA for NIK; partial cds | Hs.3628 |
| N59858 | ESTs | Hs.33032 |
| N90933 | ESTs | Hs.4867 |
| N93764 | ESTs; Moderately similar to !!!! ALU CLASS C WARNING ENTRY | Hs.10175 |
| R26124 | ESTs | Hs.24024 |
| R27957 | ESTs | Hs.24230 |
| R55470 | ESTs; Moderately similar to K02E10.2 [C.elegans] | Hs.11067 |
| T16550 | ESTs; Highly similar to vacuolar protein sorting homolog h-vps45 | Hs.6650 |
| T26674 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP | Hs.6966 |
| T57112 | "yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence." | Hs.8881 |
| T88700 | ESTs | Hs.173374 |
| T90527 | ESTs | Hs.7890 |
| W42789 | ESTs | Hs.31446 |
| W60002 | plastin 3 (T isoform) | Hs.4114 |
| W78175 | ESTs | Hs.17901 |
| W84768 | ESTs | Hs.141742 |
| W94427 | ESTs; Weakly similar to Na;K-ATPase gamma subunit | Hs.3807 |
| AA253217 | ESTs | Hs.41271 |
| AA426573 | ESTs | Hs.41135 |
| AA432374 | ESTs | Hs.48029 |
| AA446622 | ESTs | Hs.74313 |
| AA478771 | ESTs | Hs.50841 |
| AA482594 | ESTs | Hs.62684 |
| AA490588 | ESTs | Hs.43118 |
| D59570 | ESTs | Hs.17132 |
| H88157 | ESTs | Hs.41105 |
| H94648 | ESTs | Hs.41995 |
| H97538 | ESTs | Hs.42392 |
| H98670 | ESTs; Weakly similar to (defline not available 4884081) | Hs.49753 |
| N22107 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING | Hs.172241 |
| W38197 | Accession not listed in Genbank | |
| W80814 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING | Hs.196785 |
| AA287347 | ESTs | Hs.105088 |
| AA402799 | ESTs | Hs.182538 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA404418 | EST | Hs.144953 |
| AA425107 | ESTs | Hs.97016 |
| AA425435 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING | Hs.98438 |
| AA442872 | ESTs | Hs.110771 |
| AA452860 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING | Hs.197214 |
| AA488687 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING | Hs.190307 |
| AA599674 | ESTs; Weakly similar to ORF [D.melanogaster] | Hs.108115 |
| F13673 | ESTs | Hs.99769 |
| H99093 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72kD) | Hs.6179 |
| N22495 | "yw35g11.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:254276 3', mRNA sequence." | Hs.102415 |
| N23031 | myosin; heavy polypeptide 7; cardiac muscle; beta | Hs.929 |
| R15740 | carbohydrate (chondroitin 6/keratan) sulfotransferase 1 | Hs.104576 |
| R39610 | calpain; large polypeptide L2 | Hs.76288 |
| W45560 | ESTs | Hs.102541 |
| Z39833 | H.sapiens mRNA for Rho6 protein | Hs.124940 |
| Z40583 | ESTs | Hs.101259 |
| AA825437 | ESTs | |
| R66613 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone | |
| AA868063 | carbohydrate (chondroitin 6/keratan) sulfotransferase 1 | |
| AA128075 | "zl16d08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:502095 5', mRNA sequence." | |
| N66570 | ESTs | |
| AI051390 | ESTs | |
| AA627122 | ESTs | |
| X02761 | fibronectin 1 | Hs.118162 |
| AF010193 | MAD (mothers against decapentaplegic; Drosophila) homolog 7 | Hs.100602 |
| AA149044 | ESTs; Highly similar to the KIAA0195 gene is expressed | Hs.10086 |
| U82108 | solute carrier family 9 (sodium/hydrogen exchanger); isoform 3 | Hs.101813 |
| D78676 | ESTs; Moderately similar to (defline not available 4529890) | Hs.105509 |
| L35240 | enigma (LIM domain protein) | Hs.102948 |
| AA598737 | lactate dehydrogenase B | Hs.180414 |
| R69417 | ESTs | Hs.107055 |
| AA232837 | ESTs; Weakly similar to Human pre-mRNA cleavage factor I 68 kDa subunit [H.sapiens] | Hs.107125 |
| N72695 | ESTs | Hs.108557 |
| M30257 | vascular cell adhesion molecule 1 | Hs.109225 |
| M96843 | inhibitor of DNA binding 2; dominant negative helix-loop-helix protein | Hs.109617 |
| X68277 | dual specificity phosphatase 1 | Hs.171695 |
| AA292440 | myeloid differentiation primary response | Hs.110571 |
| J03040 | secreted protein; acidic; cysteine-rich (osteonectin) | Hs.111779 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA228107 | ESTs | Hs.54642 |
| AA449789 | connective tissue growth factor | Hs.75511 |
| W01367 | ESTs | Hs.170980 |
| AA610116 | ESTs; Highly similar to (defline not available 4325180) | Hs.11663 |
| AA258308 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone | Hs.165618 |
| AA460273 | Homo sapiens mRNA for KIAA0517 protein; partial cds | Hs.12372 |
| AA286710 | lymphocyte adaptor protein | Hs.13131 |
| T68873 | metallothionein 1L | Hs.143289 |
| D63476 | PAK-interacting exchange factor beta | Hs.172813 |
| M62403 | insulin-like growth factor-binding protein 4 | Hs.1516 |
| X55740 | 5' nucleotidase (CD73) | Hs.153952 |
| L10284 | calnexin | Hs.155560 |
| AA243278 | ribosomal protein; mitochondrial; L12 | Hs.109059 |
| AA430032 | pituitary tumor-transforming 1 | Hs.159626 |
| H16402 | ESTs | Hs.17121 |
| D59711 | ESTs | Hs.17132 |
| T94452 | "ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence" | |
| AA431571 | ESTs | Hs.17894 |
| R79356 | Homo sapiens mRNA for KIAA0544 protein; partial cds | Hs.19280 |
| AA280375 | ESTs | Hs.19928 |
| Z49269 | small inducible cytokine subfamily A (Cys-Cys); member 14 | Hs.20144 |
| Z41740 | ESTs | Hs.24462 |
| AA121543 | Homo sapiens mRNA for KIAA0758 protein; partial cds | Hs.22039 |
| J05008 | endothelin 1 | Hs.2271 |
| AA101878 | ESTs | Hs.22793 |
| T35341 | ESTs; Highly similar to (defline not available 4519883) [H.sapiens] | Hs.22880 |
| N87590 | ESTs | Hs.23037 |
| AA256153 | ESTs | Hs.23912 |
| W74533 | Homo sapiens mRNA for KIAA0786 protein; partial cds | Hs.24212 |
| U25997 | stanniocalcin | Hs.25590 |
| V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog | Hs.25647 |
| V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog | Hs.25647 |
| V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog | Hs.25647 |
| V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog | Hs.25647 |
| X56681 | jun D proto-oncogene | Hs.2780 |
| AA161292 | interferon; alpha-inducible protein 27 | Hs.2867 |
| AA491465 | ESTs | Hs.28792 |
| AA046593 | ESTs | Hs.28959 |
| D50914 | Human mRNA for KIAA0124 gene; partial cds | Hs.30736 |
| D45304 | ESTs | Hs.31595 |
| M90657 | transmembrane 4 superfamily member 1 | Hs.3337 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| W69127 | ESTs; Weakly similar to zinc finger protein ZNF191 [H.sapiens] | Hs.3449 |
| AA316186 | ESTs; Highly similar to (defline not available 4262136) | Hs.34549 |
| AA384503 | ESTs | Hs.179260 |
| AA136353 | ESTs | Hs.38022 |
| AA044755 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING | Hs.173705 |
| U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 | Hs.41270 |
| AA058911 | ESTs; Weakly similar to membrane glycoprotein [M.musculus] | Hs.4193 |
| AA620962 | dynein; cytoplasmic; light intermediate polypeptide 2 | Hs.44251 |
| AA285290 | small EDRK-rich factor 2 | Hs.44499 |
| X60486 | H4 histone family; member G | Hs.46423 |
| R31641 | ESTs | Hs.197148 |
| AA489190 | ESTs | Hs.48320 |
| F13782 | LIM binding domain 2 | Hs.4980 |
| AA257993 | Janus kinase 1 (a protein tyrosine kinase) | Hs.50651 |
| M24283 | intercellular adhesion molecule 1 (CD54); human rhinovirus | Hs.168383 |
| AA443114 | ESTs; Weakly similar to PIM-1 PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE [H.sapiens] | Hs.5326 |
| T35289 | casein kinase 1; alpha 1 | Hs.195206 |
| N23817 | Homo sapiens clone 23675 mRNA sequence | Hs.5807 |
| AA047151 | ESTs | Hs.5897 |
| N77151 | Homo sapiens mRNA for KIAA0799 protein; partial cds | Hs.61638 |
| AA480074 | ESTs | Hs.62206 |
| Y00787 | interleukin 8 | Hs.624 |
| T99789 | ESTs | Hs.64313 |
| W84341 | tissue inhibitor of metalloproteinase 2 | Hs.6441 |
| L09209 | amyloid beta (A4) precursor-like protein 2 | Hs.64797 |
| D12763 | interleukin 1 receptor-like 1 | Hs.66 |
| T16484 | ESTs | Hs.6607 |
| AA253193 | ESTs | Hs.6631 |
| AA432248 | ESTs | Hs.6738 |
| X82200 | stimulated trans-acting factor (50 kDa) | Hs.68054 |
| AA083572 | v-ral simian leukemia viral oncogene homolog A (ras related) | Hs.6906 |
| L00352 | low density lipoprotein receptor (familial hypercholesterolemia) | Hs.181182 |
| N75791 | ESTs | Hs.7153 |
| X57579 | H.sapiens activin beta-A subunit (exon 2) | |
| X02612 | cytochrome P450; subfamily I (aromatic compound-inducible); | Hs.72912 |
| H44631 | immediate early protein | Hs.737 |
| AA090257 | superoxide dismutase 2; mitochondrial | Hs.177781 |
| X83703 | H.sapiens mRNA for cytokine inducible nuclear protein | Hs.74019 |
| L40395 | Homo sapiens clone 23689 mRNA; complete cds | Hs.170001 |
| AA227913 | ESTs | Hs.198456 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| X52947 | gap junction protein; alpha 1; 43kD (connexin 43) | Hs.74471 |
| M11313 | alpha-2-macroglobulin | Hs.74561 |
| L14837 | tight junction protein 1 (zona occludens 1) | Hs.74614 |
| M60721 | "Human homeobox gene, complete cds" | |
| D90209 | activating transcription factor 4 (tax-responsive enhancer element | Hs.181243 |
| T67986 | "yc28e12.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82030 3' similar to gb:X14723 CLUSTERIN | Hs.75106 |
| AA148318 | Human mRNA for KIAA0069 gene; partial cds | Hs.75249 |
| U97105 | dihydropyrimidinase-like 2 | Hs.173381 |
| T25747 | H.sapiens OZF mRNA | Hs.75471 |
| K02574 | Accession not listed in Genbank | |
| D78577 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; eta polypeptide | Hs.75544 |
| X53331 | matrix Gla protein | Hs.75742 |
| S73591 | upregulated by 1;25-dihydroxyvitamin D-3 | Hs.179526 |
| X95735 | zyxin | Hs.75873 |
| L16862 | G protein-coupled receptor kinase 6 | Hs.76297 |
| U44975 | Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA; | Hs.76526 |
| M97796 | inhibitor of DNA binding 2; dominant negative helix-loop-helix | Hs.180919 |
| U86782 | 26S proteasome-associated pad1 homolog | Hs.178761 |
| AA099391 | ESTs | Hs.77310 |
| M19267 | tropomyosin 1 (alpha) | Hs.77899 |
| D29992 | tissue factor pathway inhibitor 2 | Hs.78045 |
| L19314 | phosphorylase kinase; beta | Hs.195217 |
| S78569 | laminin; alpha 4 | Hs.78672 |
| U28811 | "Human cysteine-rich fibroblast growth factor receptor (CFR-1) | |
| L77886 | protein tyrosine phosphatase; receptor type; K | Hs.79005 |
| C14407 | neuronal tissue-enriched acidic protein | Hs.79516 |
| M60278 | diphtheria toxin receptor (heparin-binding epidermal growth | Hs.799 |
| R81509 | splicing factor; arginine/serine-rich 11 | Hs.184571 |
| AA487558 | ESTs | Hs.8135 |
| D86962 | KIAA0207 gene product | Hs.81875 |
| AA478971 | disabled (Drosophila) homolog 2 (mitogen-responsive | Hs.81988 |
| D50683 | transforming growth factor; beta receptor II (70-80kD) | Hs.82028 |
| U56637 | capping protein (actin filament) muscle Z-line; alpha 1 | Hs.184270 |
| M61199 | Human cleavage signal 1 protein mRNA; complete cds | Hs.82767 |
| M28882 | "Human MUC18 glycoprotein mRNA, complete cds" | |
| X15183 | CDW52 antigen (CAMPATH-1 antigen) | Hs.180532 |
| S53911 | CD34 | Hs.85289 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| U20734 | Human transcription factor junB (junB) gene; 5' region and | Hs.198951 |
| D28235 | prostaglandin-endoperoxide synthase 2 (prostaglandin G/H | Hs.92309 |
| AA236324 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! | Hs.92381 |
| AA148923 | Homo sapiens mRNA for DEPP (decidual protein induced by | Hs.93675 |
| AA174183 | ESTs | Hs.93872 |
| AA456311 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! | Hs.93961 |
| L08069 | heat shock protein; DNAJ-like 2 | Hs.94 |
| AA452000 | ESTs | Hs.94030 |
| AA282140 | ESTs | Hs.9587 |
| J02854 | myosin regulatory light chain 2; smooth muscle isoform | Hs.9615 |
| AA442054 | phospholipase C; gamma 1 (formerly subtype 148) | Hs.993 |
| AB000450 | vaccinia related kinase 2 | |
| AB002380 | KIAA0382 protein | |
| AB003103 | proteasome (prosome; macropain) 26S subunit; non-ATPase; 12 | |
| AB004884 | tousled-like kinase 2 | |
| AF000573 | homogentisate 1;2-dioxygenase (homogentisate oxidase) | |
| AF008937 | | |
| AF009301 | similar to S. cerevisiae SSM4 | |
| AF009368 | cAMP responsive element binding protein 3 (luman) | |
| D00591 | chromosome condensation 1 | |
| D00760 | proteasome (prosome; macropain) subunit; alpha type; 2 | |
| D11139 | tissue inhibitor of metalloproteinase 1 (erythroid potentiating | |
| D14657 | KIAA0101 gene product | |
| D14878 | D123 gene product | |
| D17716 | mannosyl (alpha-1;6-)-glycoprotein beta-1;6-N-acetyl-glucosaminyltransferase | |
| D21090 | RAD23 (S. cerevisiae) homolog B | |
| D26135 | diacylglycerol kinase; gamma (90kD) | |
| D26528 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 7 (RNA helicase; | |
| D30742 | calcium/calmodulin-dependent protein kinase IV | |
| D31762 | KIAA0057 gene product; TRAM-like protein | |
| D31765 | KIAA0061 protein | |
| D31888 | KIAA0071 protein | |
| D38128 | prostaglandin I2 (prostacyclin) receptor (IP) | |
| D38500 | postmeiotic segregation increased 2-like 4 | |
| D38551 | RAD21 (S. pombe) homolog | |
| D42087 | KIAA0118 protein | |
| D49396 | antioxidant protein 1 | |
| D55640 | | |
| D63391 | platelet-activating factor acetylhydrolase; isoform Ib; gamma | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| D63477 | KIAA0143 protein | |
| D63483 | acetyl LDL receptor; SREC | |
| D64015 | TIA1 cytotoxic granule-associated RNA-binding protein-like 1 | |
| D79990 | KIAA0168 gene product | |
| D79997 | KIAA0175 gene product | |
| D80010 | KIAA0188 protein | |
| D84276 | CD38 antigen (p45) | |
| D86425 | nidogen 2 | |
| D86978 | KIAA0225 protein | |
| D87012 | Human (lambda) DNA for immunoglobin light chain | |
| D87075 | solute carrier family 23 (nucleobase transporters); member 1 | |
| D87432 | solute carrier family 7 (cationic amino acid transporter; y+ | |
| D87448 | topoisomerase (DNA) II binding protein | |
| D87845 | platelet-activating factor acetylhydrolase 2 (40kD) | |
| HG1098-HT1098 | | |
| HG2167-HT2237 | | |
| HG2415-HT2511 | | |
| HG2825-HT2949 | | |
| HG2887-HT3031 | | |
| HG4660-HT5073 | | |
| HG4704-HT5146 | | |
| HG884-HT884 | | |
| HG919-HT919 | | |
| J00212 | | |
| J04029 | keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et | |
| J04031 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methenyltetrahydrofolate cyclohydrolase; formyltetrahydrofolate | |
| J04088 | topoisomerase (DNA) II alpha (170kD) | |
| J04543 | annexin A7 | |
| L06139 | TEK tyrosine kinase; endothelial (venous malformations; multiple cutaneous and mucosal) | |
| L07540 | replication factor C (activator 1) 5 (36.5kD) | |
| L08895 | MADS box transcription enhancer factor 2; polypeptide C | |
| L11239 | gastrulation brain homeo box 1 | |
| L11353 | neurofibromin 2 (bilateral acoustic neuroma) | |
| L13773 | myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to; 2 | |
| L13800 | | |
| L14922 | replication factor C (activator 1) 1 (145kD) | |
| L15189 | heat shock 70kD protein 9B (mortalin-2) | |
| L15388 | G protein-coupled receptor kinase 5 | |
| L16895 | lysyl oxidase | |
| L27476 | tight junction protein 2 (zona occludens 2) | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| L27624 | tissue factor pathway inhibitor 2 | |
| L32976 | mitogen-activated protein kinase kinase kinase 11 | |
| L33404 | kallikrein 7 (chymotryptic; stratum corneum) | |
| L35263 | mitogen-activated protein kinase 14 | |
| L37347 | solute carrier family 11 (proton-coupled divalent metal ion | |
| L40371 | thyroid hormone receptor interactor 4 | |
| L40391 | Homo sapiens (clone s153) mRNA fragment | |
| L41607 | glucosaminyl (N-acetyl) transferase 2; I-branching enzyme | |
| L77566 | DiGeorge syndrome critical region gene DGSI | |
| M13928 | aminolevulinate; delta-; dehydratase | |
| M13928 | aminolevulinate; delta-; dehydratase | |
| M14016 | uroporphyrinogen decarboxylase | |
| M14219 | decorin | |
| M15796 | proliferating cell nuclear antigen | |
| M21305 | Human alpha satellite and satellite 3 junction DNA sequence | |
| M22092 | | |
| M22898 | tumor protein p53 (Li-Fraumeni syndrome) | |
| M22995 | RAP1A; member of RAS oncogene family | |
| M23379 | RAS p21 protein activator (GTPase activating protein) 1 | |
| M24364 | major histocompatibility complex; class II; DQ beta 1 | |
| M24400 | chymotrypsinogen B1 | |
| M25753 | cyclin B1 | |
| M27691 | cAMP responsive element binding protein 1 | |
| M28213 | RAB2; member RAS oncogene family | |
| M29550 | protein phosphatase 3 (formerly 2B); catalytic subunit; alpha | |
| M29971 | O-6-methylguanine-DNA methyltransferase | |
| M30269 | nidogen (enactin) | |
| M31158 | protein kinase; cAMP-dependent; regulatory; type II; beta | |
| M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | |
| M31210 | endothelial differentiation; sphingolipid G-protein-coupled receptor; 1 | |
| M55420 | Epsilon ; IgE | |
| M59979 | prostaglandin-endoperoxide synthase 1 (prostaglandin G/H | |
| M62810 | transcription factor 6-like 1 (mitochondrial transcription factor | |
| M63838 | interferon; gamma-inducible protein 16 | |
| M64710 | Human CNP gene for C-type natriuretic peptide | |
| M68874 | | |
| M74524 | ubiquitin-conjugating enzyme E2A (RAD6 homolog) | |
| M80254 | peptidylprolyl isomerase F (cyclophilin F) | |
| M81780 | sphingomyelin phosphodiesterase 1; acid lysosomal (acid | |
| M81780 | sphingomyelin phosphodiesterase 1; acid lysosomal (acid | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| M81780 | sphingomyelin phosphodiesterase 1; acid lysosomal (acid | |
| M81780 | Homo sapiens acid sphingomyelinase (SMPD1) gene; complete cds; ORF's 1-3; complete cds's | |
| M81780 | Homo sapiens acid sphingomyelinase (SMPD1) gene; complete cds; ORF's 1-3; complete cds's | |
| M83822 | cell division cycle 4-like | |
| M86934 | DNA segment; numerous copies; expressed probes (GS1 gene) | |
| M87338 | replication factor C (activator 1) 2 (40kD) | |
| M96326 | azurocidin 1 (cationic antimicrobial protein 37) | |
| M96954 | TIA1 cytotoxic granule-associated RNA-binding protein-like 1 | |
| M98833 | Friend leukemia virus integration 1 | |
| S66793 | arrestin 3; retinal (X-arrestin) | |
| S72370 | pyruvate carboxylase | |
| S78569 | laminin; alpha 4 | |
| S79873 | lysosomal-associated membrane protein 2 | |
| S83325 | aspartate beta-hydroxylase | |
| S83364 | | |
| S83365 | | |
| U01212 | olfactory marker protein (symbol provisional) | |
| U01922 | translocase of inner mitochondrial membrane 8 (yeast) homolog A | |
| U02556 | t-complex-associated-testis-expressed 1-like | |
| U02680 | protein tyrosine kinase 9 | |
| U03272 | fibrillin 2(congenital contractural arachnodactyly) | |
| U04209 | microfibrillar-associated protein 1 | |
| U05237 | fetal Alzheimer antigen | |
| U07225 | purinergic receptor P2Y; G-protein coupled; 2 | |
| U07620 | mitogen-activated protein kinase 10 | |
| U09759 | mitogen-activated protein kinase 9 | |
| U09820 | alpha thalassemia/mental retardation syndrome X-linked | |
| U11313 | sterol carrier protein 2 | |
| U14518 | centromere protein A (17kD) | |
| U14575 | protein phosphatase 1; regulatory (inhibitor) subunit 8 | |
| U15173 | BCL2/adenovirus E1B 19kD-interacting protein 2 | |
| U15932 | dual specificity phosphatase 5 | |
| U18291 | CDC16 (cell division cycle 16; S. cerevisiae; homolog) | |
| U18300 | damage-specific DNA binding protein 2 (48kD) | |
| U18383 | nuclear respiratory factor 1 | |
| U20536 | caspase 6; apoptosis-related cysteine protease | |
| U21551 | branched chain aminotransferase 1; cytosolic | |
| U23028 | eukaryotic translation initiation factor 2B; subunit 5 (epsilon; | |
| U23752 | SRY (sex-determining region Y)-box 11 | |
| U25435 | transcriptional repressor | |
| U25997 | stanniocalcin | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| U28251 | zinc finger protein 169 | |
| U28831 | | |
| U30245 | | |
| U32315 | syntaxin 3A | |
| U32439 | regulator of G-protein signalling 7 | |
| U32849 | N-myc (and STAT) interactor | |
| U35139 | necdin (mouse) homolog | |
| U36764 | eukaryotic translation initiation factor 3; subunit 2 (beta; 36kD) | |
| U39400 | chromosome 11 open reading frame 4 | |
| U39657 | mitogen-activated protein kinase kinase 6 | |
| U41344 | proline arginine-rich end leucine-rich repeat protein | |
| U41766 | a disintegrin and metalloproteinase domain 9 (meltrin gamma) | |
| U41813 | homeo box A9 | |
| U41815 | nucleoporin 98kD | |
| U43286 | selenophosphate synthetase 2 | |
| U44378 | MAD (mothers against decapentaplegic; Drosophila) homolog 4 | |
| U44754 | small nuclear RNA activating complex; polypeptide 1; 43kD | |
| U47011 | fibroblast growth factor 8 (androgen-induced) | |
| U47011 | fibroblast growth factor 8 (androgen-induced) | |
| U47011 | fibroblast growth factor 8 (androgen-induced) | |
| U47011 | fibroblast growth factor 8 (androgen-induced) | |
| U47077 | protein kinase; DNA-activated; catalytic polypeptide | |
| U48251 | protein kinase C binding protein 1 | |
| U50535 | Human BRCA2 region; mRNA sequence CG006 | |
| U56833 | von Hippel-Lindau binding protein 1 | |
| U58091 | cullin 4B | |
| U58837 | cyclic nucleotide gated channel beta 1 | |
| U59289 | cadherin 13; H-cadherin (heart) | |
| U59863 | TRAF family member-associated NFKB activator | |
| U67122 | ubiquitin-like 1 (sentrin) | |
| U67319 | caspase 7; apoptosis-related cysteine protease | |
| U68019 | MAD (mothers against decapentaplegic; Drosophila) homolog 3 | |
| U69611 | a disintegrin and metalloproteinase domain 17 (tumor necrosis factor; alpha; converting enzyme) | |
| U70322 | karyopherin (importin) beta 2 | |
| U73524 | ATP/GTP-binding protein | |
| U79267 | protein phosphatase 4; regulatory subunit 1 | |
| U79291 | Human clone 23721 mRNA sequence | |
| U82671 | Homo sapiens clone LM1955 H105e3 gene; partial cds | |
| U82671 | zinc finger protein 185 (LIM domain) | |
| U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine | |
| U90914 | carboxypeptidase D | |
| U91316 | cytosolic acyl coenzyme A thioester hydrolase | |
| U91932 | adaptor-related protein complex 3; sigma 1 subunit | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| U96131 | Homo sapiens HPV16 E1 protein binding protein mRNA; | |
| U97018 | echinoderm microtubule-associated protein-like | |
| U97188 | IGF-II mRNA-binding protein 3 | |
| V00503 | collagen; type I; alpha 2 | |
| X04327 | 2;3-bisphosphoglycerate mutase | |
| X06389 | synaptophysin | |
| X07496 | apolipoprotein A-I | |
| X07820 | matrix metalloproteinase 10 (stromelysin 2) | |
| X14787 | thrombospondin 1 | |
| X15525 | acid phosphatase 2; lysosomal | |
| X16396 | methylene tetrahydrofolate dehydrogenase (NAD+ dependent); methenyltetrahydrofolate cyclohydrolase | |
| X16609 | ankyrin 1; erythrocytic | |
| X53586 | integrin; alpha 6 | |
| X53586 | integrin; alpha 6 | |
| X53793 | multifunctional polypeptide similar to SAICAR synthetase and AIR | |
| X54936 | placental growth factor; vascular endothelial growth factor-related | |
| X55740 | 5' nucleotidase (CD73) | |
| X57025 | insulin-like growth factor 1 (somatomedin C) | |
| X60673 | adenylate kinase 3 | |
| X60673 | adenylate kinase 3 | |
| X60708 | dipeptidylpeptidase IV (CD26; adenosine deaminase complexing | |
| X62048 | wee1+ (S. pombe) homolog | |
| X63097 | Rhesus blood group; D antigen | |
| X63563 | polymerase (RNA) II (DNA directed) polypeptide B (140kD) | |
| X64037 | general transcription factor IIF; polypeptide 1 (74kD subunit) | |
| X69636 | hect domain and RLD 2 | |
| X69878 | fms-related tyrosine kinase 4 | |
| X70649 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 | |
| X72841 | retinoblastoma-binding protein 7 | |
| X74987 | ATP-binding cassette; sub-family E (OABP); member 1 | |
| X83107 | BMX non-receptor tyrosine kinase | |
| X84194 | acylphosphatase 1; erythrocyte (common) type | |
| X85753 | cyclin-dependent kinase 8 | |
| X87870 | hepatocyte nuclear factor 4; alpha | |
| X89066 | transient receptor potential channel 1 | |
| X89398 | uracil-DNA glycosylase | |
| X89398 | uracil-DNA glycosylase | |
| X89399 | RAS p21 protein activator (GTPase activating protein) 3 | |
| X89426 | endothelial cell-specific molecule 1 | |
| X91247 | thioredoxin reductase 1 | |
| X91648 | H.sapiens mRNA for pur alpha extended 3'untranslated region | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| X92098 | coated vesicle membrane protein | |
| X92110 | H.sapiens mRNA for hcgVIII protein | |
| X94703 | RAB28; member RAS oncogene family | |
| X96506 | DR1-associated protein 1 (negative cofactor 2 alpha) | |
| X97230 | killer cell immunoglobulin-like receptor; three domains; long | |
| X98263 | M-phase phosphoprotein 6 | |
| X98296 | ubiquitin specific protease 9; X chromosome (Drosophila fat | |
| X99584 | SMT3 (suppressor of mif two 3; yeast) homolog 1 | |
| Y00264 | amyloid beta (A4) precursor protein (protease nexin-II; Alzheimer | |
| Y07566 | Ric (Drosophila)-like; expressed in many tissues | |
| Y07759 | myosin VA (heavy polypeptide 12; myoxin) | |
| Y07827 | butyrophilin; subfamily 3; member A1 | |
| Y07867 | Pirin | |
| Y09443 | alkylglycerone phosphate synthase | |
| Y09858 | H.sapiens mRNA for unknown protein | |
| Y12394 | karyopherin alpha 3 (importin alpha 4) | |
| Z11559 | iron-responsive element binding protein 1 | |
| Z11695 | mitogen-activated protein kinase 1 | |
| Z15005 | centromere protein E (312kD) | |
| Z46261 | H3 histone family; member A | |
| AA011243 | poly(rC)-binding protein 2 | |
| AA018418 | ESTs; Weakly similar to type-1 protein phosphatase skeletal muscle glycogen targeting subunit [H.sapiens] | |
| AA018758 | ESTs | |
| AA018804 | Homo sapiens clone 23675 mRNA sequence | |
| AA031993 | SUMO-1 activating enzyme subunit 2 | |
| AA044217 | ESTs; Weakly similar to collagen alpha 2(I) chain [R.norvegicus] | |
| AA046548 | SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1 | |
| AA057447 | ESTs; Moderately similar to alternatively spliced product using | |
| AA058376 | Sjogren syndrome antigen A2 (60kD; ribonucleoprotein | |
| AA083572 | v-ral simian leukemia viral oncogene homolog A (ras related) | |
| AA085696 | | |
| AA088744 | ESTs | |
| AA089688 | EST | |
| AA091284 | ESTs; Highly similar to HSPC030 [H.sapiens] | |
| AA092700 | ESTs | |
| AA092968 | ESTs | |
| AA094800 | eukaryotic translation initiation factor 3; subunit 7 (zeta; 66/67kD) | |
| AA100219 | ESTs | |
| AA114885 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA129547 | met proto-oncogene (hepatocyte growth factor receptor) | |
| AA133016 | ESTs | |
| AA149507 | homolog of mouse quaking QKI (KH domain RNA binding protein) | |
| AA151005 | sperm surface protein | |
| AA187101 | | |
| AA195179 | eukaryotic translation initiation factor 4A; isoform 2 | |
| AA203138 | low density lipoprotein receptor (familial hypercholesterolemia) | |
| AA203645 | Arg/Abl-interacting protein ArgBP2 | |
| AA206236 | | |
| AA227621 | ESTs; Weakly similar to weak similarity to collagens [C.elegans] | |
| AA248283 | ESTs; Weakly similar to prostate-specific transglutaminase | |
| AA249611 | SH3-binding domain glutamic acid-rich protein | |
| AA282640 | ubiquitination factor E4B (homologous to yeast UFD2) | |
| AA287199 | KIAA0081 protein | |
| AA313990 | DKFZP564M112 protein | |
| AA314256 | ESTs; Highly similar to CGI-94 protein [H.sapiens] | |
| AA314389 | ADP-ribosylation factor-like 5 | |
| AA324364 | ESTs | |
| AA329211 | NS1-associated protein 1 | |
| AA399187 | DKFZP434A043 protein | |
| AA421079 | ESTs; Weakly similar to Sox-like transcriptional factor [H.sapiens] | |
| AA422029 | ESTs | |
| AA425230 | Ras-GTPase-activating protein SH3-domain-binding protein | |
| AA447052 | KIAA0251 protein | |
| AA452000 | Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone | |
| AA456687 | ESTs | |
| AA487015 | Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone | |
| AB002326 | Human mRNA for KIAA0328 gene; partial cds | |
| -BioB-3 | | |
| C01527 | ESTs | |
| C01714 | serum-inducible kinase | |
| C01811 | Homo sapiens clone 24921 mRNA sequence | |
| C02352 | ESTs; Highly similar to CGI-121 protein [H.sapiens] | |
| C02375 | ESTs | |
| C14448 | EST | |
| D16611 | coproporphyrinogen oxidase (coproporphyria; harderoporphyria) | |
| D25216 | KIAA0014 gene product | |
| D31352 | ESTs | |
| D58024 | ESTs; Weakly similar to KIAA0768 protein [H.sapiens] | |
| D80897 | KIAA1036 protein | |
| D82614 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| D87845 | platelet-activating factor acetylhydrolase 2 (40kD) | |
| D89377 | msh (Drosophila) homeo box homolog 2 | |
| H06583 | cAMP responsive element binding protein-like 2 | |
| H40732 | ESTs | |
| H46617 | ESTs | |
| H56731 | ESTs | |
| H75570 | ESTs | |
| H78886 | ESTs | |
| H81241 | Kruppel-like factor 8 | |
| L36531 | integrin; alpha 8 | |
| M63154 | gastric intrinsic factor (vitamin B synthesis) | |
| M63180 | threonyl-tRNA synthetase | |
| M91504 | ESTs | |
| N56191 | protocadherin 68 | |
| N78483 | ESTs; Weakly similar to F20D12.3 gene product [C.elegans] | |
| N79268 | zinc finger protein 198 | |
| R14652 | Homo sapiens PAC clone DJ0872F07 from 7q31 | |
| R20459 | ESTs | |
| R22303 | ESTs; Weakly similar to putative p150 [H.sapiens] | |
| R33779 | ESTs; Weakly similar to p40 [H.sapiens] | |
| R36553 | ESTs; Weakly similar to KIAA0681 protein [H.sapiens] | |
| R64534 | ESTs | |
| R66475 | ESTs | |
| R70621 | KIAA0896 protein | |
| R79356 | KIAA0544 protein | |
| R84933 | ESTs | |
| AA007160 | Homo sapiens mRNA; cDNA DKFZp564D016 (from clone | |
| AA007234 | ESTs | |
| AA018409 | ESTs | |
| AA025351 | ESTs | |
| AA027168 | KIAA0955 protein | |
| AA027317 | ESTs | |
| AA029423 | ESTs; Weakly similar to PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE [H.sapiens] | |
| AA031357 | ESTs; Weakly similar to N-WASP [H.sapiens] | |
| AA045136 | ESTs | |
| AA053400 | ESTs | |
| AA055829 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | |
| AA065217 | ESTs | |
| AA116054 | ESTs; Weakly similar to KIAA0638 protein [H.sapiens] | |
| AA126311 | ESTs | |
| AA129390 | ESTs | |
| AA130273 | ESTs; Weakly similar to hypothetical protein; similar to | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA142919 | ESTs | |
| AA150205 | Kruppel-like factor 7 (ubiquitous) | |
| AA176867 | ESTs | |
| AA180321 | Homo sapiens (clone S164) mRNA; 3' end of cds | |
| AA180487 | transforming; acidic coiled-coil containing protein 1 | |
| AA187634 | eukaryotic translation initiation factor 3; subunit 1 (alpha; 35kD) | |
| AA195399 | ESTs | |
| AA234717 | ESTs | |
| AA234743 | ESTs | |
| AA234957 | myotubularin related protein 1 | |
| AA235604 | Homo sapiens clone 25007 mRNA sequence | |
| AA236559 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING | |
| AA242868 | ESTs; Weakly similar to house-keeping protein [M.musculus] | |
| AA251776 | jun D proto-oncogene | |
| AA251909 | budding uninhibited by benzimidazoles 1 (yeast homolog); beta | |
| AA252672 | diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2 | |
| AA256157 | ESTs | |
| AA256680 | Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone | |
| AA258873 | ESTs | |
| AA262727 | KIAA1033 protein | |
| AA281451 | DKFZP564A043 protein | |
| AA281545 | nuclear receptor co-repressor 1 | |
| AA282069 | KIAA0603 gene product | |
| AA283044 | ESTs | |
| AA283930 | ESTs | |
| AA284755 | CDW52 antigen (CAMPATH-1 antigen) | |
| AA291268 | DKFZP586L0724 protein | |
| AA291927 | ESTs | |
| AA343514 | ESTs | |
| AA398109 | ESTs | |
| AA405737 | ESTs | |
| AA406610 | ESTs | |
| AA411465 | ESTs; Moderately similar to HMG-box transcription factor | |
| AA416886 | Homo sapiens mRNA; cDNA DKFZp564C1563 (from clone | |
| AA424013 | Homo sapiens clone 23767 and 23782 mRNA sequences | |
| AA424148 | DKFZP434I116 protein | |
| AA424558 | phosducin-like | |
| AA424961 | similar to S. cerevisiae SSM4 | |
| AA425367 | ESTs | |
| AA425921 | ESTs | |
| AA426220 | KIAA0523 protein | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA427735 | ESTs | |
| AA430673 | ESTs | |
| AA432248 | ESTs | |
| AA435896 | ESTs | |
| AA436705 | KIAA0766 gene product | |
| AA446561 | KIAA0470 gene product | |
| AA448238 | KIAA0915 protein | |
| AA448688 | ESTs; Weakly similar to KIAA0638 protein [H.sapiens] | |
| AA449756 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | |
| AA450303 | ESTs | |
| AA452411 | ESTs; Highly similar to mediator [H.sapiens] | |
| AA454566 | hemoglobin; gamma G | |
| AA454667 | ESTs | |
| AA456437 | ESTs | |
| AA456646 | ESTs | |
| AA456826 | ESTs | |
| AA456981 | ESTs | |
| AA458959 | ESTs | |
| AA459950 | ESTs | |
| AA460449 | ESTs; Highly similar to phosphoserine aminotransferase | |
| AA463910 | ESTs | |
| AA464603 | ESTs | |
| AA464606 | MRS1 protein | |
| AA465093 | TIA1 cytotoxic granule-associated RNA-binding protein | |
| AA465692 | KIAA0648 protein | |
| AA476473 | triple functional domain (PTPRF interacting) | |
| AA478109 | ESTs | |
| AA478474 | ESTs | |
| AA480889 | ESTs | |
| AA485223 | ESTs | |
| AA485254 | ESTs | |
| AA486183 | ESTs; Weakly similar to similar to oxysterol-binding proteins | |
| AA496936 | ESTs | |
| AA598589 | ESTs | |
| AA598831 | ESTs | |
| AA600150 | ESTs | |
| AA608545 | RAD51 (S. cerevisiae) homolog (E coli RecA homolog) | |
| AA609210 | ESTs | |
| AA610108 | ESTs; Highly similar to CGI-124 protein [H.sapiens] | |
| AA620582 | ESTs; Weakly similar to KIAA0869 protein [H.sapiens] | |
| AA621239 | ESTs; Highly similar to ALG-2 interacting protein AIP1 | |
| AA621714 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA621718 | ESTs; Moderately similar to CGI-74 protein [H.sapiens] | |
| D19673 | ESTs | |
| D25755 | ESTs | |
| D51095 | DKFZP586E1621 protein | |
| D60272 | ESTs; Weakly similar to macrophage lectin 2 [H.sapiens] | |
| T08879 | cathepsin F | |
| T34527 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | |
| T40327 | lung resistance-related protein | |
| T62771 | nucleophosmin/nucleoplasmin; 3 | |
| T63174 | Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone | |
| T83444 | KIAA0887 protein | |
| T93641 | ESTs | |
| U48263 | prepronociceptin | |
| U49065 | interleukin 1 receptor-like 2 | |
| U79300 | Human clone 23629 mRNA sequence | |
| U88573 | NBR2 | |
| U93867 | polymerase (RNA) III (DNA directed) (62kD) | |
| W01094 | ESTs | |
| W01568 | ESTs | |
| W26853 | cartilage oligomeric matrix protein (pseudoachondroplasia; epiphyseal dysplasia 1; multiple) | |
| W27179 | BCL2/adenovirus E1B 19kD-interacting protein 3-like | |
| W27965 | EST | |
| W36280 | NS1-associated protein 1 | |
| W47063 | ESTs | |
| W79060 | isocitrate dehydrogenase 2 (NADP+); mitochondrial | |
| W88550 | KIAA1058 protein | |
| X60486 | H4 histone family; member G | |
| X78931 | zinc finger protein 272 | |
| Z14077 | YY1 transcription factor | |
| AA002147 | EST | |
| AA004711 | ESTs | |
| AA010383 | EST | |
| AA015761 | ESTs | |
| AA018772 | ESTs | |
| AA021473 | EST | |
| AA024835 | potassium voltage-gated channel; delayed-rectifier; subfamily S; | |
| AA025858 | Homo sapiens mRNA; cDNA DKFZp586B1024 (from clone | |
| AA027229 | ESTs; Weakly similar to F45E12.5 [C.elegans] | |
| AA029428 | ESTs | |
| AA035143 | ESTs | |
| AA035237 | butyrate response factor 2 (EGF-response factor 2) | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA039347 | EST | |
| AA040740 | ESTs | |
| AA041551 | ESTs | |
| AA045513 | ESTs | |
| AA045745 | ESTs | |
| AA055348 | ESTs | |
| AA056582 | KIAA0372 gene product | |
| AA056697 | ESTs | |
| AA056746 | EST | |
| AA057678 | ESTs | |
| AA058681 | ESTs | |
| AA058686 | ESTs | |
| AA062840 | | |
| AA064859 | | |
| AA065069 | | |
| AA069923 | | |
| AA070799 | zinc finger protein 6 (CMPX1) | |
| AA070815 | | |
| AA075374 | | |
| AA076382 | | |
| AA078787 | ESTs | |
| AA078986 | | |
| AA079393 | | |
| AA079487 | | |
| AA083207 | EST | |
| AA083256 | | |
| AA084415 | | |
| AA085274 | | |
| AA088678 | ESTs | |
| AA100925 | stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 | |
| AA101255 | Homo sapiens mRNA for H-2K binding factor-2; complete cds | |
| AA126474 | stanniocalcin 2 | |
| AA127017 | ESTs | |
| AA129968 | ESTs; Weakly similar to PROTEIN PHOSPHATASE PP2A; 130 KD REGULATORY SUBUNIT [H.sapiens] | |
| AA130240 | ESTs | |
| AA131866 | ESTs; Weakly similar to DY3.6 [C.elegans] | |
| AA132039 | ESTs | |
| AA132983 | DKFZP586G1517 protein | |
| AA133250 | ESTs | |
| AA133583 | high-mobility group (nonhistone chromosomal) protein isoform I-C | |
| AA135941 | ESTs | |
| AA148650 | | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA151110 | ESTs | |
| AA155754 | EST | |
| AA156125 | ESTs; Moderately similar to hedgehog-interacting protein [M.musculus] | |
| AA156289 | ESTs | |
| AA156997 | ESTs | |
| AA157291 | EST | |
| AA157293 | ESTs | |
| AA164293 | ESTs | |
| AA164676 | ESTs; Weakly similar to weak similarity to S. cerevisiae intracellular protein transport protein US)1 [C.elegans] | |
| AA167375 | KIAA0530 protein | |
| AA167550 | Homo sapiens mRNA; cDNA DKFZp564M113 (from clone | |
| AA176589 | EST | |
| AA180448 | EST | |
| AA187144 | endothelin 1 | |
| AA189170 | ESTs | |
| AA192757 | ESTs | |
| AA205650 | ESTs | |
| AA233342 | ESTs; Weakly similar to WD40 protein Ciao 1 [H.sapiens] | |
| AA233472 | ESTs | |
| AA234110 | ESTs | |
| D80981 | ESTs | |
| F01660 | ESTs | |
| F02206 | EST; Highly similar to ether-a-go-go-related protein [H.sapiens] | |
| F02208 | ESTs | |
| F02544 | ESTs | |
| F03918 | ESTs | |
| F04258 | pyrophosphatase (inorganic) | |
| F04600 | ESTs | |
| F08998 | ESTs | |
| F09605 | ESTs | |
| F11115 | ESTs | |
| H06371 | Homo sapiens clone 24993 mRNA sequence | |
| H10995 | Homo sapiens mRNA full length insert cDNA clone EUROIMAGE | |
| H11938 | ESTs; Highly similar to histone acetyltransferase [H.sapiens] | |
| H16568 | ESTs | |
| H16772 | ESTs | |
| H18951 | ESTs; Moderately similar to dJ1163J1.1 [H.sapiens] | |
| H20859 | ESTs | |
| H23747 | ESTs | |
| H38087 | ESTs; Weakly similar to NG22 [H.sapiens] | |
| H40331 | ESTs | |
| H40567 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| H46966 | ESTs | |
| H56640 | ESTs | |
| H57154 | ESTs; Weakly similar to organic anion transporter 1 [H.sapiens] | |
| H96712 | ESTs | |
| N20814 | ESTs | |
| N25249 | synaptosomal-associated protein; 23kD | |
| N27100 | keratin 5 (epidermolysis bullosa simplex; | |
| N39616 | RNA (guanine-7-) methyltransferase | |
| N48982 | ESTs | |
| N51957 | ESTs | |
| N52271 | LIM protein (similar to rat protein kinase C-binding enigma) | |
| N59435 | ESTs; Highly similar to CGI-112 protein [H.sapiens] | |
| N64139 | ESTs; Weakly similar to large tumor suppressor 1 [H.sapiens] | |
| N66981 | ESTs | |
| N68640 | ESTs | |
| N69352 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15 | |
| N95226 | KIAA0758 protein | |
| R00138 | ESTs | |
| R07998 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | |
| R08929 | ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7) | |
| R10307 | ESTs | |
| R33354 | ESTs | |
| R36083 | ESTs | |
| R37938 | KIAA0440 protein | |
| R39330 | | |
| R40816 | cullin 4A | |
| R43162 | ESTs | |
| R45698 | ESTs; Weakly similar to cAMP inducible 2 protein [M.musculus] | |
| R54554 | ESTs | |
| R68425 | ESTs | |
| R68568 | ATX1 (antioxidant protein 1; yeast) homolog 1 | |
| R68763 | ESTs | |
| R70467 | ESTs | |
| R73565 | Homo sapiens mRNA; cDNA DKFZp564M113 (from clone | |
| R73640 | ESTs | |
| R78376 | EST | |
| R92453 | EST | |
| T03865 | ESTs | |
| T03872 | ESTs | |
| T10072 | ESTs | |
| T10080 | ESTs | |
| T10132 | KIAA0478 gene product | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| T15343 | ESTs | |
| T23457 | ESTs | |
| T23555 | ESTs | |
| T23670 | ESTs | |
| T23948 | ESTs | |
| T33464 | ESTs | |
| T34413 | ESTs | |
| T34611 | ESTs | |
| T40920 | ESTs | |
| T55182 | ESTs; Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens] | |
| T77453 | ESTs | |
| T84039 | ESTs | |
| T86458 | ESTs | |
| T87693 | EST | |
| T89350 | ESTs | |
| T90945 | ESTs | |
| T90987 | ESTs | |
| T91863 | ESTs | |
| T91881 | KIAA0563 gene product | |
| T93783 | ESTs | |
| T96687 | ESTs | |
| T96944 | Homo sapiens mRNA; cDNA DKFZp434H132 (from clone | |
| T97307 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING | |
| T97764 | ESTs | |
| W48817 | ESTs | |
| W58343 | DKFZP586B2420 protein | |
| W59949 | ESTs; Moderately similar to GTP-BINDING PROTEIN TC10 | |
| W74644 | ESTs | |
| W74761 | ESTs; Highly similar to ubiquitin-conjugating enzyme HBUCE1 | |
| W74802 | ESTs | |
| W81205 | ESTs | |
| W81237 | ESTs | |
| W90146 | ESTs | |
| W92798 | ESTs | |
| Z38412 | EST | |
| Z38709 | inositol 1;4;5-triphosphate receptor; type 2 | |
| Z38904 | ESTs; Weakly similar to KIAA0970 protein [H.sapiens] | |
| Z39103 | core-binding factor; runt domain; alpha subunit 2; translocated to; | |
| Z39930 | calreticulin | |
| Z39939 | ESTs | |
| Z40012 | NCK-associated protein 1 | |
| Z40377 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| Z40820 | ESTs | |
| Z41680 | Homo sapiens mRNA; cDNA DKFZp566P013 (from clone | |
| -BioB-3 | | |
| AA005112 | LIM domain only 7 | |
| AA005432 | DKFZP547E2110 protein | |
| AA010163 | upstream regulatory element binding protein 1 | |
| AA026356 | ESTs | |
| AA026901 | ESTs | |
| AA036867 | ESTs; Weakly similar to coded for by C. elegans cDNA yk30b3.5 | |
| AA044644 | lymphocyte-specific protein 1 | |
| AA046426 | Cdc42 effector protein 3 | |
| AA054515 | ESTs; Weakly similar to prostate-specific transglutaminase | |
| AA084162 | | |
| AA085749 | ATP binding protein associated with cell differentiation | |
| AA098874 | DKFZP434I116 protein | |
| AA101056 | | |
| AA102746 | ESTs | |
| AA114250 | KIAA0512 gene product | |
| AA126561 | stanniocalcin | |
| AA128980 | ESTs | |
| AA129757 | ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 | |
| AA129921 | S-adenosylhomocysteine hydrolase-like 1 | |
| AA133331 | KIAA0741 gene product | |
| AA135958 | ESTs | |
| AA136524 | eukaryotic translation elongation factor 1 alpha 1 | |
| AA147044 | ESTs; Weakly similar to !!!! ALU CLASS C WARNING ENTRY !!!! | |
| AA148885 | minichromosome maintenance deficient (S. cerevisiae) 4 | |
| AA150043 | ESTs | |
| AA151621 | ESTs | |
| AA155743 | ferritin; light polypeptide | |
| AA156335 | ESTs | |
| AA156336 | nuclear receptor co-repressor 1 | |
| AA159181 | ESTs; Weakly similar to Lpa8p [S.cerevisiae] | |
| AA159825 | ESTs; Weakly similar to ORF YNL227c [S.cerevisiae] | |
| AA234185 | ESTs | |
| AA234929 | ESTs | |
| AA234935 | ESTs | |
| AA236359 | ESTs | |
| AA236466 | ESTs | |
| AA236535 | Human clone 23654 mRNA sequence | |
| AA236935 | Human normal keratinocyte mRNA | |
| AA236942 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA237018 | ESTs | |
| AA237025 | ESTs | |
| AA242751 | KIAA0903 protein | |
| AA242760 | | |
| AA242763 | CDC14 (cell division cycle 14; S. cerevisiae) homolog B | |
| AA242809 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | |
| AA243133 | serine/threonine kinase 15 | |
| AA243495 | lectin; mannose-binding; 1 | |
| AA243706 | ESTs | |
| AA250848 | ESTs | |
| AA250868 | ESTs | |
| AA251152 | ESTs | |
| AA251544 | ESTs | |
| AA251792 | fatty-acid-Coenzyme A ligase; long-chain 4 | |
| AA252063 | BH-protocadherin (brain-heart) | |
| AA252144 | ESTs | |
| AA252524 | | |
| AA253461 | ESTs | |
| AA255522 | ESTs; Weakly similar to INHIBITOR OF APOPTOSIS PROTEIN 1 | |
| AA256468 | ESTs | |
| AA256528 | ESTs | |
| AA257976 | ESTs | |
| AA258296 | KIAA0579 protein | |
| AA258409 | myelin protein zero-like 1 | |
| AA258421 | hypothetical protein | |
| AA262077 | aldehyde dehydrogenase 5 family; member A1 | |
| AA278650 | ESTs; Weakly similar to similar to the beta transducin family | |
| AA278766 | ESTs | |
| AA279667 | natural killer-tumor recognition sequence | |
| AA280791 | eukaryotic translation initiation factor 5 | |
| AA280819 | MADS box transcription enhancer factor 2; polypeptide C | |
| AA280828 | Homo sapiens mRNA; cDNA DKFZp586M141 (from clone | |
| AA282195 | ESTs; Weakly similar to Unknown [H.sapiens] | |
| AA283127 | Homo sapiens clone LM1955 H105e3 gene; partial cds | |
| AA284694 | nucleoporin-like protein 1 | |
| AA291137 | ESTs | |
| AA291708 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING | |
| AA293495 | chromosome 8 open reading frame 1 | |
| AA347193 | ESTs | |
| AA398474 | Homo sapiens mRNA; cDNA DKFZp586H051 (from clone | |
| AA398512 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA400277 | ESTs | |
| AA400896 | ESTs | |
| AA404494 | CTP synthase | |
| AA410345 | ESTs; Weakly similar to junctional adhesion molecule [H.sapiens] | |
| AA416733 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SC WARNING | |
| AA425154 | ESTs | |
| AA426573 | ESTs; Moderately similar to endomucin [M.musculus] | |
| AA431418 | N-acetylglucosaminidase; alpha- (Sanfilippo disease IIIB) | |
| AA436182 | Human DNA sequence from clone 44A20 on chromosome 6q23.1-24.3. Contains a gene for a novel protein similar to MTHFD1 (methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methenyltetrahydrofolate cyclohydrolase; | |
| AA437099 | ESTs | |
| AA446585 | ESTs | |
| AA446887 | ESTs | |
| AA447224 | ESTs; Weakly similar to cDNA EST CEESW54F comes from this | |
| AA447709 | ESTs; Moderately similar to putative transcription factor CA150 | |
| AA453624 | deoxynucleotidyltransferase; terminal | |
| AA455044 | ESTs | |
| AA456045 | ESTs | |
| AA460454 | ESTs; Weakly similar to KIAA0512 protein [H.sapiens] | |
| AA476494 | ESTs; Weakly similar to KIAA0512 protein [H.sapiens] | |
| AA476738 | leucine rich repeat (in FLII) interacting protein 1 | |
| AA481422 | Homo sapiens mRNA for H-2K binding factor-2; complete cds | |
| AA482269 | integral membrane protein 1 | |
| AA482595 | ESTs; Weakly similar to F25B5.3 [C.elegans] | |
| AA485084 | ESTs | |
| AA485431 | ESTs | |
| AA489057 | stromal antigen 2 | |
| AA489638 | DKFZP564M2423 protein | |
| AA491000 | Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone | |
| AA491250 | ESTs | |
| AA505133 | solute carrier family 2 (facilitated glucose transporter); member 3 | |
| AA598447 | exportin; tRNA (nuclear export receptor for tRNAs) | |
| AA599243 | general transcription factor IIIA | |
| AA599574 | lipase; endothelial | |
| AA600153 | DEK oncogene (DNA binding) | |
| AA609309 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | |
| AA609710 | Human chromosome 3p21.1 gene sequence | |
| AA610068 | PIBF1 gene product | |
| AA621399 | ESTs | |
| AA621752 | 26S proteasome-associated pad1 homolog | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| C21523 | ESTs | |
| D12160 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING | |
| D19708 | ESTs | |
| D25801 | ESTs; Highly similar to KIAA0445 protein [H.sapiens] | |
| D45652 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif; 4; aggrecan 1 | |
| D60208 | ESTs | |
| D80504 | zinc finger protein 198 | |
| F03010 | myeloid/lymphoid or mixed-lineage leukemia 2 | |
| F04247 | ESTs | |
| F10966 | Homo sapiens mRNA; cDNA DKFZp434M196 (from clone | |
| F13700 | ribonuclease P; 40kD subunit | |
| H05063 | ESTs; Weakly similar to /prediction | |
| H16758 | erythropoietin receptor | |
| H17315 | EST | |
| H22556 | putative translation initiation factor | |
| H22566 | ESTs | |
| H48459 | KIAA0186 gene product | |
| H53073 | | |
| H56559 | KIAA0601 protein | |
| H57957 | EST | |
| H64938 | ESTs | |
| H64973 | ESTs | |
| H69535 | ESTs | |
| H73110 | ESTs | |
| H81783 | ESTs | |
| H86259 | Homo sapiens chromosome 19; cosmid R32611 | |
| H88353 | ESTs; Weakly similar to line-1 protein ORF2 [H.sapiens] | |
| H88639 | YY1-associated factor 2 | |
| H88675 | nuclear receptor co-repressor 1 | |
| H93708 | sperm specific antigen 2 | |
| N22107 | ESTs | |
| N24046 | ESTs | |
| N27028 | ESTs | |
| N30205 | ESTs | |
| N30621 | ESTs | |
| N33258 | nuclear receptor co-repressor 1 | |
| N33390 | EST | |
| N40180 | EST | |
| N45198 | EST; Highly similar to similar to Cdc14B1 phosphatase [H.sapiens] | |
| N45979 | SH3 domain protein 1B | |
| N48325 | EST | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| N48913 | ESTs | |
| N49394 | KIAA0716 gene product | |
| N50656 | ESTs; Highly similar to mosaic protein LR11 [H.sapiens] | |
| N50721 | signal sequence receptor; gamma (translocon-associated protein | |
| N53143 | Homo sapiens clone 25218 mRNA sequence | |
| N53359 | ESTs; Weakly similar to beta-TrCP protein E3RS-IkappaB | |
| N55326 | ESTs | |
| N55493 | | |
| N57493 | EST | |
| N62955 | ESTs; Weakly similar to KIAA0396 [H.sapiens] | |
| N63520 | EST | |
| N63604 | ESTs | |
| N64166 | frizzled (Drosophila) homolog 7 | |
| N64168 | ESTs | |
| N64191 | ESTs | |
| N66845 | ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! | |
| N67135 | ESTs | |
| N67295 | ESTs | |
| N68399 | H2B histone family; member N | |
| N68963 | ESTs | |
| N69331 | peptidylprolyl isomerase C (cyclophilin C) | |
| N70777 | ESTs | |
| N71364 | ESTs | |
| N71545 | ESTs | |
| N71571 | ESTs | |
| N74456 | EST | |
| N75594 | ESTs | |
| N79035 | ESTs | |
| N80279 | hypothetical protein | |
| N91797 | ESTs | |
| N92454 | karyopherin (importin) beta 1 | |
| N94581 | actin; beta | |
| N94746 | ESTs | |
| N98238 | ESTs | |
| R02384 | ESTs | |
| R16833 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | |
| R41828 | myosin VA (heavy polypeptide 12; myoxin) | |
| R43203 | EST | |
| R46395 | DKFZP566A0946 protein | |
| R58863 | ESTs | |
| R78248 | ESTs; Weakly similar to KIAA0970 protein [H.sapiens] | |
| T11483 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| T16896 | ESTs | |
| T23820 | cyclin T2 | |
| T30222 | ESTs; Moderately similar to tetracycline transporter-like protein | |
| W15275 | Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone | |
| W38194 | | |
| W42414 | MAD (mothers against decapentaplegic; Drosophila) homolog 3 | |
| W46577 | endothelial cell-specific molecule 1 | |
| W49632 | Human clone 23908 mRNA sequence | |
| W57613 | ESTs | |
| W57759 | EST | |
| W61118 | ESTs | |
| W65344 | ESTs; Moderately similar to hypothetical protein [H.sapiens] | |
| W69216 | ESTs | |
| W69379 | Homo sapiens mRNA; cDNA DKFZp586D0923 (from clone | |
| W86728 | ESTs | |
| Z38499 | MKP-1 like protein tyrosine phosphatase | |
| Z38630 | bladder cancer related protein (10kD) | |
| Z39494 | ESTs | |
| Z39623 | ESTs | |
| Z40071 | BMX non-receptor tyrosine kinase | |
| Z40174 | ESTs | |
| Z40182 | EST | |
| Z40904 | EST | |
| AA166965 | ESTs | |
| AA167500 | EST | |
| AA169599 | ESTs | |
| AA171724 | ESTs; Weakly similar to ORF YNL059c [S.cerevisiae] | |
| AA171739 | ESTs | |
| AA177105 | ESTs; Weakly similar to MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens] | |
| AA182626 | ESTs | |
| AA186324 | cell cycle progression 8 protein | |
| AA192099 | zinc finger protein 148 (pHZ-52) | |
| AA192173 | ESTs | |
| AA192415 | ESTs | |
| AA192553 | ESTs; Highly similar to RGC-32 [R.norvegicus] | |
| AA194851 | ESTs | |
| AA195520 | ESTs | |
| AA196300 | ESTs; Weakly similar to alternatively spliced product using exon | |
| AA196517 | protease; serine; 15 | |
| AA196549 | ESTs | |
| AA196721 | | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA196729 | ESTs | |
| AA196979 | ESTs; Weakly similar to protease [H.sapiens] | |
| AA206828 | | |
| AA207123 | immunoglobulin superfamily; member 3 | |
| AA214539 | TIA1 cytotoxic granule-associated RNA-binding protein | |
| AA226914 | nuclear receptor subfamily 2; group C; member 1 | |
| AA227260 | Zic family member 3 (odd-paired Drosophila homolog; heterotaxy | |
| AA227469 | EST | |
| AA233122 | ESTs; Highly similar to multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform | |
| AA233334 | Machado-Joseph disease (spinocerebellar ataxia 3; olivopontocerebellar ataxia 3; autosomal dominant; ataxin 3) | |
| AA233347 | zinc finger protein 216 | |
| AA233519 | ESTs; Weakly similar to evectin-1 [R.norvegicus] | |
| AA233714 | Apg12 (autophagy 12; S. cerevisiae)-like | |
| AA233796 | eukaryotic translation initiation factor 4E | |
| AA235050 | ESTs | |
| AA235704 | ESTs; Weakly similar to Wiscott-Aldrich Syndrome protein | |
| AA236031 | ESTs | |
| AA236352 | ESTs | |
| AA236390 | ESTs | |
| AA236453 | ESTs | |
| AA243370 | EST | |
| AA250947 | ESTs | |
| AA251083 | ESTs | |
| AA251113 | ESTs | |
| AA251973 | ESTs | |
| AA252023 | ESTs; Weakly similar to HRIHFB2157 [H.sapiens] | |
| AA252414 | ESTs | |
| AA252650 | mitogen-activated protein kinase kinase 7 | |
| AA255523 | ESTs | |
| AA258128 | ESTs | |
| AA262105 | Homo sapiens mRNA; cDNA DKFZp564L1916 (from clone | |
| AA262107 | ESTs | |
| AA262235 | ESTs | |
| AA278298 | M-phase phosphoprotein 1 | |
| AA278529 | serine/threonine kinase 18 | |
| AA278721 | ESTs | |
| AA280036 | eukaryotic translation initiation factor 4A; isoform 2 | |
| AA280648 | ESTs; Weakly similar to rab-related GTP-binding protein | |
| AA280738 | ESTs | |
| AA280794 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA280837 | ESTs | |
| AA280886 | ESTs | |
| AA280934 | ESTs | |
| AA281535 | KIAA0879 protein | |
| AA281797 | general transcription factor IIH; polypeptide 2 (44kD subunit) | |
| AA282047 | ESTs | |
| AA283002 | zinc finger protein 187 | |
| AA283709 | calpain like protease | |
| AA283902 | ESTs | |
| AA284108 | Human DNA from chromosome 19-specific cosmid F25965; | |
| AA284109 | Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene; an unknown putative gene; a pseudogene with high similarity to part | |
| AA284371 | interleukin 13 receptor, alpha 1 | |
| AA284744 | ESTs; Highly similar to prefoldin subunit 2 [M.musculus] | |
| AA284784 | mitochondrial ribosome recycling factor | |
| AA284840 | ESTs | |
| AA286844 | ESTs | |
| AA287032 | ESTs | |
| AA287038 | ESTs | |
| AA287546 | ESTs | |
| AA287553 | ESTs | |
| AA287556 | ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! | |
| AA287564 | IDN3 protein | |
| AA291015 | CDC7 (cell division cycle 7; S. cerevisiae; homolog)-like 1 | |
| AA291716 | ESTs | |
| AA291749 | estrogen receptor 1 | |
| AA293656 | ESTs | |
| AA302430 | Human DNA sequence from clone 141H5 on chromosome Xq22.1-23. Contains parts of a novel Chordin LIKE protein with von Willebrand factor type C domains. Contains ESTs; STSs and | |
| AA302809 | EST | |
| AA302820 | purinergic receptor P2X; ligand-gated ion channel; 4 | |
| AA310499 | ESTs | |
| AA321890 | | |
| AA340589 | EST | |
| AA340622 | ESTs | |
| AA342457 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING | |
| AA342828 | glycoprotein V (platelet) | |
| AA342864 | ESTs | |
| AA342973 | ESTs | |
| AA346495 | ESTs | |
| AA347573 | fibronectin leucine rich transmembrane protein 2 | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA347614 | ESTs | |
| AA347717 | ESTs | |
| AA348913 | ESTs | |
| AA349647 | EST | |
| AA349773 | ESTs | |
| AA350541 | ESTs | |
| AA357159 | EST | |
| AA357172 | ESTs | |
| AA369856 | vacuolar protein sorting 41 (yeast homolog) | |
| AA370132 | EST | |
| AA370472 | ESTs | |
| AA370867 | ESTs | |
| AA377296 | ESTs | |
| AA383902 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING | |
| AA385934 | EST; Highly similar to predicted using Genefinder [C.elegans] | |
| AA386255 | EST | |
| AA386260 | EST | |
| AA386266 | ESTs; Weakly similar to M6a [H.sapiens] | |
| AA398014 | ESTs | |
| AA398222 | ESTs | |
| AA398235 | ESTs | |
| AA398348 | ESTs | |
| AA398482 | EST | |
| AA398504 | ESTs | |
| AA398505 | ESTs | |
| AA398507 | nucleoporin 50kD | |
| AA398523 | ESTs | |
| AA398625 | ESTs | |
| AA398632 | ESTs | |
| AA398633 | ESTs | |
| AA398894 | ESTs | |
| AA398895 | EST | |
| AA398900 | ESTs | |
| AA398904 | EST | |
| AA399122 | ESTs; Weakly similar to mitochondrial citrate transport protein | |
| AA399371 | ESTs; Weakly similar to zinc finger protein SALL1 [H.sapiens] | |
| AA399373 | ESTs; Highly similar to KIAA0568 protein [H.sapiens] | |
| AA399441 | ESTs | |
| AA399636 | ESTs | |
| AA399640 | ESTs | |
| AA399680 | ESTs | |
| AA400080 | ESTs | |
| AA400262 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA400725 | ESTs | |
| AA400748 | Homo sapiens mRNA; cDNA DKFZp434D024 (from clone | |
| AA400780 | ESTs | |
| AA401631 | ESTs | |
| AA401688 | ESTs | |
| AA401695 | EST | |
| AA402227 | ESTs; Weakly similar to TROPOMODULIN [H.sapiens] | |
| AA402329 | phosphodiesterase 4A; cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) | |
| AA402398 | ESTs | |
| AA402449 | EST | |
| AA402468 | ESTs | |
| AA403268 | ESTs | |
| AA403314 | ESTs | |
| AA404229 | EST | |
| AA404260 | ESTs | |
| AA404271 | glutamate receptor; ionotropic; kainate 1 | |
| AA405026 | ESTs | |
| AA405182 | ESTs | |
| AA405237 | | |
| AA406061 | EST | |
| AA406063 | ESTs | |
| AA406070 | EST | |
| AA406137 | EST | |
| AA406335 | ESTs | |
| AA411801 | KIAA0307 gene product | |
| AA411804 | ESTs | |
| AA411833 | ESTs; Highly similar to Trad [H.sapiens] | |
| AA412219 | ESTs | |
| AA412259 | ESTs | |
| AA412497 | EST | |
| AA412498 | ESTs | |
| AA416586 | ESTs | |
| AA416867 | EST | |
| AA416874 | ESTs | |
| AA421133 | ESTs | |
| AA421138 | EST | |
| AA422079 | ESTs; Weakly similar to RAR-RESPONSIVE PROTEIN TIG1 | |
| AA423837 | ESTs | |
| AA424328 | ESTs | |
| AA424339 | ESTs | |
| AA424469 | ESTs | |
| AA424502 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA425004 | ESTs | |
| AA425734 | ESTs; Weakly similar to hypothetical protein [H.sapiens] | |
| AA425887 | ESTs | |
| AA426456 | ESTs | |
| AA427396 | ESTs | |
| AA427555 | KIAA0203 gene product | |
| AA428218 | ESTs | |
| AA428242 | transcription factor 9 (binds GC-rich sequences) | |
| AA428281 | EST | |
| AA428865 | EST | |
| AA428994 | ESTs | |
| AA429666 | ESTs | |
| AA430181 | ESTs | |
| AA430184 | ATP/GTP-binding protein | |
| AA431288 | CD3D antigen; delta polypeptide (TiT3 complex) | |
| AA431293 | ESTs | |
| AA431478 | ESTs | |
| AA431492 | EST | |
| AA431732 | EST | |
| AA432278 | ESTs | |
| AA434411 | ESTs | |
| AA435512 | ESTs | |
| AA435698 | ESTs | |
| AA435711 | KIAA0712 gene product | |
| AA435815 | Clk-associating RS-cyclophilin | |
| AA435842 | ESTs | |
| AA436475 | ESTs | |
| AA436489 | ESTs | |
| AA442060 | ESTs | |
| AA442079 | ESTs | |
| AA443151 | ESTs; Weakly similar to weak similarity with quinone | |
| AA446133 | ESTs | |
| AA447145 | Homo sapiens KIAA0399 mRNA; partial cds | |
| AA447398 | EST | |
| AA447643 | ESTs | |
| AA447742 | dynein; axonemal; heavy polypeptide 17-like | |
| AA448226 | | |
| AA448825 | EST | |
| AA449444 | ESTs | |
| AA450087 | regulator of Gz-selective protein signaling | |
| AA450211 | EST | |
| AA450244 | ESTs | |
| AA452123 | ESTs; Weakly similar to T-complex protein 10A [H.sapiens] | |
| AA452155 | zinc finger protein 198 | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA452156 | EST | |
| AA453036 | ESTs; Weakly similar to similar to molybdoterin biosynthesis | |
| AA453526 | ESTs | |
| AA454085 | EST | |
| AA454103 | ESTs | |
| AA454642 | ESTs | |
| AA454935 | nuclear respiratory factor 1 | |
| AA456323 | ESTs | |
| AA457395 | ESTs | |
| AA458850 | | |
| AA459662 | ESTs | |
| AA459668 | 3-hydroxyisobutyryl-Coenzyme A hydrolase | |
| AA459679 | ESTs; Weakly similar to The KIAA0191 gene is expressed | |
| AA459702 | ESTs | |
| AA460017 | ESTs; Weakly similar to diaphanous-related formin [M.musculus] | |
| AA460324 | ESTs | |
| AA461509 | ESTs; Weakly similar to putative p150 [H.sapiens] | |
| AA464414 | ESTs | |
| AA464428 | ESTs | |
| AA470084 | ESTs | |
| AA476606 | ESTs | |
| AA478521 | ESTs | |
| AA478523 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING | |
| AA479949 | RAB2; member RAS oncogene family | |
| AA481252 | oncogene TC21 | |
| AA485351 | KIAA1067 protein | |
| AA487264 | ESTs | |
| AA489072 | KIAA0870 protein | |
| AA489630 | KIAA0665 gene product | |
| AA490225 | ESTs | |
| AA490227 | ESTs | |
| AA490255 | ESTs | |
| AA490890 | ESTs | |
| AA490916 | ESTs | |
| AA490925 | epilepsy; progressive myoclonic epilepsy; type 2 gene; Lafora | |
| AA490955 | ESTs; Weakly similar to bullous pemphigoid antigen [M.musculus] | |
| AA495812 | ESTs | |
| AA495824 | ESTs | |
| AA496369 | ESTs | |
| AA504125 | ESTs | |
| AA521473 | SEC10 (S. cerevisiae)-like 1 | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA598440 | EST | |
| AA598899 | Homo sapiens mRNA; cDNA DKFZp564D036 (from clone | |
| AA599244 | KIAA0530 protein | |
| AA599694 | KIAA0133 gene product | |
| AA600037 | ESTs | |
| AA609135 | ESTs | |
| AA609582 | katanin p60 (ATPase-containing) subunit A 1 | |
| AA609684 | ESTs | |
| AA609839 | 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like | |
| AA609862 | RNA-binding protein gene with multiple splicing | |
| AA620423 | EST | |
| AA620747 | ESTs | |
| AA621364 | ESTs | |
| C20653 | ESTs | |
| D20085 | ESTs; Weakly similar to KIAA0742 protein [H.sapiens] | |
| D20749 | ESTs | |
| D51285 | ESTs | |
| D59972 | cullin 5 | |
| F04112 | ESTs | |
| F13604 | ESTs | |
| H01662 | ESTs | |
| H05135 | ESTs | |
| H12245 | | |
| H22842 | EST | |
| H30894 | ESTs | |
| H43442 | leucyl-tRNA synthetase; mitochondrial | |
| H45996 | putative G protein-coupled receptor | |
| H69281 | ESTs | |
| H69485 | ESTs | |
| H69899 | ESTs; Moderately similar to unknown [H.sapiens] | |
| H70627 | ESTs; Weakly similar to !!!! ALU CLASS E WARNING ENTRY !!!! | |
| H73050 | Rhesus blood group; D antigen | |
| H73260 | ESTs | |
| H77531 | HIR (histone cell cycle regulation defective; S. cerevisiae) | |
| H80552 | EST | |
| H80737 | lysyl oxidase | |
| H93412 | ESTs; Weakly similar to ORF YGR101w [S.cerevisiae] | |
| H94892 | v-ral simian leukemia viral oncogene homolog A (ras related) | |
| H95643 | neurotrophic tyrosine kinase; receptor; type 1 | |
| H96552 | ESTs | |
| H97146 | ESTs; Highly similar to G protein-coupled receptor kinase 6; | |
| H99131 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| H99462 | ribosomal protein; mitochondrial; L12 | |
| H99837 | ESTs | |
| N22140 | ESTs; Weakly similar to beta-tubulin [H.sapiens] | |
| N22197 | Sec23-interacting protein p125 | |
| N23756 | solute carrier family 23 (nucleobase transporters); member 1 | |
| N24134 | eukaryotic translation initiation factor 1A; Y chromosome | |
| N24195 | novel centrosomal protein RanBPM | |
| N26739 | DKFZP564B147 protein | |
| N27098 | EST | |
| N27637 | ESTs | |
| N33090 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (Dbp5; yeast; | |
| N35967 | serine/threonine kinase 24 (Ste20; yeast homolog) | |
| N38959 | chaperonin containing TCP1; subunit 2 (beta) | |
| N39069 | ESTs | |
| N46441 | ESTs | |
| N48270 | ESTs | |
| N48365 | ESTs | |
| N51316 | ESTs | |
| N51499 | A kinase (PRKA) anchor protein 2 | |
| N53976 | ESTs | |
| N54157 | ESTs | |
| N54300 | ESTs | |
| N54831 | ESTs | |
| N59849 | ESTs | |
| N62132 | ESTs | |
| N62375 | EST | |
| N63138 | ESTs | |
| N63172 | cell division cycle 42 (GTP-binding protein; 25kD) | |
| N63772 | novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7 | |
| N63787 | sema domain; immunoglobulin domain (Ig); short basic domain; | |
| N68168 | | |
| N68201 | ESTs | |
| N68300 | ESTs | |
| N68321 | EST | |
| N69575 | EST | |
| N75007 | ESTs; Moderately similar to KIAA1004 protein [H.sapiens] | |
| N75542 | transcription factor 4 | |
| N90066 | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl | |
| N91246 | ESTs | |
| N92751 | ESTs; Weakly similar to MICROTUBULE-ASSOCIATED | |
| N93214 | KIAA0318 protein | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| N99148 | ESTs; Weakly similar to ZINC FINGER PROTEIN 83 [H.sapiens] | |
| R07876 | ESTs; Weakly similar to unknown [S.cerevisiae] | |
| R10865 | alpha-fetoprotein | |
| R11056 | ESTs | |
| R11488 | ESTs | |
| R22947 | ESTs | |
| R23930 | ESTs; Highly similar to prediabetic NOD sera-reactive autoantigen | |
| R26589 | ESTs | |
| R37588 | RAB2; member RAS oncogene family-like | |
| R37613 | Homo sapiens clone 25027 mRNA sequence | |
| R38398 | Homo sapiens clone 23758 mRNA sequence | |
| R39179 | ESTs | |
| R40923 | ESTs | |
| R41179 | Human mRNA for KIAA0328 gene; partial cds | |
| R41294 | ESTs | |
| R42307 | early development regulator 2 (homolog of polyhomeotic 2) | |
| R43189 | ESTs | |
| R43306 | ESTs | |
| R44357 | ESTs; Weakly similar to cDNA EST EMBL:T01421 comes from | |
| R44519 | EST; Moderately similar to Pro-Pol-dUTPase polyprotein | |
| R45088 | | |
| R47948 | ESTs | |
| R51524 | ESTs | |
| R54950 | ESTs | |
| R55241 | ESTs | |
| R59585 | ESTs | |
| R60044 | ESTs; Highly similar to BETA-CATENIN [H.sapiens] | |
| R60872 | ESTs | |
| R66690 | ESTs | |
| R67266 | exostoses (multiple)-like 1 | |
| R73588 | ESTs | |
| R79403 | ESTs | |
| R87647 | ESTs | |
| R93622 | eukaryotic translation initiation factor 2; subunit 2 (beta; 38kD ) | |
| R99599 | heterogeneous nuclear ribonucleoprotein U (scaffold attachment | |
| R99612 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING | |
| T02888 | | |
| T03170 | EST | |
| T10465 | | |
| T15418 | EST | |
| T15597 | KIAA0661 gene product | |
| T15652 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| T16898 | ash2 (absent; small; or homeotic; Drosophila; homolog)-like | |
| T26644 | ESTs; Weakly similar to zinc finger protein [H.sapiens] | |
| T40841 | ESTs | |
| T47566 | | |
| T50116 | | |
| T50145 | | |
| T58615 | ESTs | |
| T59940 | ESTs | |
| T63595 | ESTs | |
| T64891 | | |
| T64924 | ESTs | |
| T64933 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | |
| T68875 | | |
| T69027 | ESTs | |
| T69924 | | |
| T70353 | ESTs | |
| T79780 | ESTs; Weakly similar to CGI-69 protein [H.sapiens] | |
| T79951 | ESTs | |
| T80174 | ESTs; Moderately similar to similar to NEDD-4 [H.sapiens] | |
| T80622 | ESTs; Weakly similar to envelope [H.sapiens] | |
| T85352 | ESTs | |
| T85373 | ESTs | |
| T86284 | ESTs | |
| T89579 | transcription factor Dp-1 | |
| T90360 | ESTs | |
| T94328 | ESTs | |
| T95590 | | |
| T97257 | ESTs | |
| T97599 | ESTs | |
| T97620 | ESTs | |
| T97775 | EST | |
| T98152 | fibrillin 2(congenital contractural arachnodactyly) | |
| W31479 | ESTs | |
| W37999 | ESTs | |
| W38240 | | |
| W40150 | chondroitin sulfate proteoglycan 6 (bamacan) | |
| W45435 | KIAA0784 protein | |
| W58202 | ESTs | |
| W58344 | ESTs | |
| W58650 | ESTs | |
| W68736 | Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3; EC 1.6.99.3; CI-MLRQ); Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112; | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| W69106 | chromobox homolog 3 (Drosophila HP1 gamma) | |
| W69111 | ESTs | |
| W69385 | nuclear mitotic apparatus protein 1 | |
| W69399 | H1 histone family; member 0 | |
| W69459 | sex comb on midleg (Drosophila)-like 1 | |
| W72424 | S100 calcium-binding protein A9 (calgranulin B) | |
| W72724 | ESTs | |
| W72834 | ESTs | |
| W73955 | Homo sapiens chromosome 19; cosmid R26445 | |
| W74701 | ESTs | |
| W76540 | DKFZP564G2022 protein | |
| W79397 | ESTs | |
| W85888 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING | |
| W86038 | ESTs | |
| W86881 | ESTs | |
| W87804 | ESTs | |
| W88942 | | |
| W90022 | ESTs; Highly similar to LECT2 precursor [H.sapiens] | |
| W92272 | chromodomain helicase DNA binding protein 3 | |
| W92764 | tumor necrosis factor; alpha-induced protein 6 | |
| W93040 | Homo sapiens paired mesoderm homeo box 1 (PMX1); mRNA | |
| W93092 | neutral sphingomyelinase (N-SMase) activation associated factor | |
| W93227 | EST | |
| W93523 | ESTs | |
| W93659 | ESTs | |
| W94003 | ESTs | |
| W94401 | ESTs | |
| W94688 | perilipin | |
| W94787 | destrin (actin depolymerizing factor) | |
| Z38294 | ESTs | |
| Z38311 | ESTs | |
| Z38465 | ESTs | |
| Z38525 | ESTs | |
| Z38538 | ESTs | |
| Z38551 | ESTs | |
| Z38783 | Ca2+-dependent activator protein for secretion | |
| Z39113 | ESTs | |
| Z39255 | YDD19 protein | |
| Z39591 | EST | |
| Z39783 | ESTs; Weakly similar to K01H12.1 [C.elegans] | |
| Z39920 | ESTs; Weakly similar to NADH-CYTOCHROME B5 REDUCTASE | |
| Z40166 | ESTs | |
| Z40388 | ESTs | |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| Z40646 | ESTs | |
| Z41697 | ESTs | |
| Z99349 | ESTs | |
| Z99394 | zinc finger protein 36 (KOX 18) | |

TABLE 4

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| D86425 | Homo sapiens mRNA for nidogen-2 | Hs.82733 |
| D86983 | Human mRNA for KIAA0230 gene; partial cds | Hs.118893 |
| HG1098-HT1098 | Cystatin D | |
| HG1103-HT1103 | Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related | |
| HG3342-HT3519 | Id1 | |
| J03764 | plasminogen activator inhibitor; type I | Hs.82085 |
| L06797 | chemokine (C-X-C motif); receptor 4 (fusin) | Hs.89414 |
| L15388 | Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds | Hs.211569 |
| L20971 | phosphodiesterase 4B; cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) | Hs.188 |
| L35545 | endothelial cell protein C/activated protein C receptor | Hs.82353 |
| L76380 | calcitonin receptor-like | Hs.152175 |
| M21305 | Human alpha satellite and satellite 3 junction DNA sequence | Hs.247946 |
| M24736 | selectin E (endothelial adhesion molecule 1) | Hs.89546 |
| M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | Hs.2050 |
| M31551 | plasminogen activator inhibitor; type II (arginine-serpin) | Hs.75716 |
| M32334 | intercellular adhesion molecule 2 | Hs.83733 |
| M61916 | laminin; beta 1 | Hs.82124 |
| M68874 | Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds | |
| M74719 | transcription factor 4 | Hs.75356 |
| M92934 | connective tissue growth factor | Hs.75511 |
| M94856 | fatty acid binding protein 5 (psoriasis-associated) | Hs.153179 |
| U03057 | singed (Drosophila)-like (sea urchin fascin homolog like) | Hs.118400 |
| U03877 | EGF-containing fibulin-like extracellular matrix protein 1 | Hs.76224 |
| U18300 | damage-specific DNA binding protein 2 (48kD) | Hs.77602 |
| U27109 | Human prepromultimerin mRNA; complete cds | Hs.32934 |
| U31384 | guanine nucleotide binding protein 11 | Hs.83381 |
| U33053 | protein kinase C-like 1 | Hs.2499 |
| U59423 | MAD (mothers against decapentaplegic; Drosophila) homolog 1 | Hs.79067 |
| U70322 | karyopherin (importin) beta 2 | Hs.168075 |
| U81607 | kinase scaffold protein gravin | Hs.788 |
| U83463 | syndecan binding protein (syntenin) | Hs.8180 |
| U89942 | lysyl oxidase-like 2 | Hs.83354 |
| X04729 | Human mRNA for plasminogen activator inhibitor type 1 N-terminus | |
| X06256 | integrin; alpha 5 (fibronectin receptor; alpha polypeptide) | Hs.149609 |
| X07820 | matrix metalloproteinase 10 (stromelysin 2) | Hs.2258 |
| X54925 | matrix metalloproteinase 1 (interstitial collagenase) | Hs.83169 |
| X54936 | placental growth factor; vascular endothelial growth factor-related protein | Hs.2894 |
| X60957 | tyrosine kinase with immunoglobulin and epidermal growth factor homology domains | Hs.78824 |
| X67235 | hematopoietically expressed homeobox | Hs.118651 |
| X67951 | proliferation-associated gene A (natural killer-enhancing factor A) | Hs.180909 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| X69910 | H.sapiens p63 mRNA for transmembrane protein | Hs.74368 |
| X79981 | cadherin 5; VE-cadherin (vascular epithelium) | Hs.76206 |
| Z18951 | caveolin 1; caveolae protein; 22kD | Hs.247266 |
| AA187101 | zp61b6.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:624659 5', mRNA sequence | |
| N24990 | ESTs | Hs.26418 |
| R81003 | Homo sapiens serine protease mRNA; complete cds | Hs.154737 |
| AA025351 | ESTs | Hs.134797 |
| AA027168 | ESTs | Hs.10031 |
| AA040465 | ESTs | Hs.8728 |
| AA045136 | ESTs | Hs.22575 |
| AA054087 | phospholipase A2; group IVC (cytosolic; calcium-independent) | Hs.18858 |
| AA071089 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] | Hs.187932 |
| AA085918 | H.sapiens HUNKI mRNA | Hs.247482 |
| AA187490 | ESTs | Hs.21941 |
| AA227926 | ESTs | Hs.6682 |
| AA234743 | ESTs | Hs.22120 |
| AA236559 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] | Hs.8768 |
| AA292694 | ESTs | Hs.3807 |
| AA398243 | ESTs; Moderately similar to (defline not available 3694664) [H.sapiens] | Hs.21806 |
| AA406363 | ESTs | Hs.30822 |
| AA411465 | ESTs | Hs.8619 |
| AA412284 | poliovirus receptor | Hs.171844 |
| AA423987 | ESTs | Hs.7567 |
| AA425309 | ESTs | Hs.33287 |
| AA435896 | ESTs | Hs.18397 |
| AA448238 | Homo sapiens mRNA for KIAA0915 protein; complete cds | Hs.16714 |
| AA478778 | ESTs | Hs.16450 |
| AA621714 | ESTs | Hs.25338 |
| D51069 | Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds | Hs.211579 |
| T34527 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | Hs.80120 |
| U97519 | podocalyxin-like | Hs.16426 |
| AA127221 | ESTs | Hs.71059 |
| AA132983 | ESTs; Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE; CYTOPLASMIC [H.sapiens] | Hs.44155 |
| AA135606 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens] | Hs.189384 |
| AA156125 | ESTs | Hs.72116 |
| AA179845 | RAB6 interacting; kinesin-like (rabkinesin6) | Hs.73625 |
| AA232645 | ESTs | Hs.42699 |
| F10399 | ESTs | Hs.14763 |
| H16772 | ESTs | Hs.31444 |
| N39584 | ESTs | Hs.17404 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| N52006 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | Hs.80120 |
| N53375 | Homer; neuronal immediate early gene; 3 | Hs.166146 |
| N54067 | Homo sapiens mRNA for NIK; partial cds | Hs.3628 |
| N64436 | ESTs | Hs.20813 |
| R26892 | ESTs | Hs.221434 |
| T33637 | ESTs | Hs.6841 |
| T57112 | yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence. | |
| W80763 | ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus] | Hs.3849 |
| AA046808 | ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S27 [H.sapiens] | Hs.108957 |
| AA253217 | ESTs | Hs.41271 |
| AA255991 | ESTs | Hs.175319 |
| AA258138 | ESTs | Hs.88297 |
| AA426573 | ESTs | Hs.41135 |
| AA443793 | ESTs | Hs.94761 |
| AA490588 | ESTs | Hs.43118 |
| AA496257 | ESTs; Weakly similar to (defline not available 3513303) [H.sapiens] | Hs.72165 |
| AA609717 | ESTs; Weakly similar to MICROTUBULE-ASSOCIATED PROTEIN 1B [H.sapiens] | Hs.66048 |
| D59570 | ESTs | Hs.17132 |
| F13787 | ESTs | Hs.58596 |
| H88157 | ESTs | Hs.41105 |
| H98988 | ESTs | Hs.42612 |
| N34287 | unc5 (C.elegans homolog) C | Hs.44553 |
| N52090 | EST | Hs.47420 |
| N66845 | ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens] | Hs.165411 |
| N68905 | small inducible cytokine A5 (RANTES) | |
| R32894 | ESTs | Hs.45514 |
| R61715 | ESTs | Hs.138237 |
| R71234 | yi54c08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143054 3' similar to gb\|M87908\|HUMALNE32 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:S41458 ROD | |
| R98105 | yr30g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206852 3', mRNA sequence. | |
| T97186 | small inducible cytokine A5 (RANTES) | |
| W80814 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens] | Hs.193700 |
| AA404418 | EST | Hs.144953 |
| AA405747 | ESTs; Moderately similar to HMG-box transcription factor [M.musculus] | Hs.97865 |
| AA488687 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | Hs.190307 |
| AA599143 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | |
| AA608588 | ESTs | Hs.193634 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA608751 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] | Hs.244904 |
| C13961 | EST | Hs.210115 |
| D60302 | ESTs | Hs.108977 |
| H94892 | v-raf simian leukemia viral oncogene homolog A (ras related) | Hs.6906 |
| N93521 | transcription factor 4 | Hs.241362 |
| N95477 | ESTs | Hs.102943 |
| R60044 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | Hs.106706 |
| R70506 | ESTs; Moderately similar to transformation-related protein [H.sapiens] | Hs.107159 |
| T91518 | ye20f05.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118305 3' similar to contains Alu repetitive element;contains | |
| T95333 | ESTs; Weakly similar to Strabismus [D.melanogaster] | Hs.122730 |
| R45630 | ESTs; Highly similar to KIAA0372 [H.sapiens] | Hs.170098 |
| R20839 | yg05c07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31444 5', mRNA sequence. | |
| R23858 | ESTs; Moderately similar to envelope protein [H.sapiens] | Hs.23986 |
| AI024874 | ESTs; Weakly similar to (defline not available 3882257) [H.sapiens] | Hs.57958 |
| W26247 | U5 snRNP-specific protein (220 kD); ortholog of S. cerevisiae Prp8p | Hs.6413 |
| AA856990 | ESTs | Hs.125058 |
| AA136653 | ESTs | |
| AA358869 | ESTs; Highly similar to SEC13-RELATED PROTEIN [H.sapiens] | Hs.227949 |
| AI123976 | ESTs | Hs.105689 |
| AI369384 | arylsulfatase D | |
| AA379500 | ESTs | Hs.193155 |
| R49693 | ESTs | Hs.107708 |
| AA195678 | Homo sapiens mRNA for KIAA0465 protein; partial cds | Hs.108258 |
| M30257 | vascular cell adhesion molecule 1 | Hs.109225 |
| AA028131 | ESTs | Hs.110342 |
| M10321 | Human von Willebrand factor mRNA, 3' end | Hs.110802 |
| J03040 | secreted protein; acidic; cysteine-rich (osteonectin) | Hs.111779 |
| M86933 | amelogenin (Y chromosome) | Hs.1238 |
| AA012933 | tubulin-specific chaperone d | Hs.241687 |
| AA286710 | lymphocyte adaptor protein | Hs.13131 |
| AA243278 | ribosomal protein; mitochondrial; L12 | Hs.109059 |
| D59711 | ESTs | Hs.237289 |
| T94452 | ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence | Hs.241207 |
| AA053400 | ESTs | Hs.241227 |
| AA370302 | Homo sapiens mRNA; cDNA DKFZp586I1518 (from clone DKFZp586I1518) | Hs.21739 |
| J05008 | endothelin 1 | Hs.2271 |
| U85193 | nuclear factor I/B | Hs.33287 |
| AA256153 | ESTs | Hs.23912 |
| X83107 | BMX non-receptor tyrosine kinase | Hs.27372 |
| AA046593 | ESTs | Hs.28959 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA410480 | ESTs | Hs.30089 |
| D45304 | ESTs | Hs.31595 |
| M90657 | transmembrane 4 superfamily member 1 | Hs.3337 |
| AA010163 | upstream regulatory element binding protein 1 | Hs.3383 |
| AA136353 | ESTs | Hs.38022 |
| Y07867 | pirin | Hs.38842 |
| U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 | Hs.41270 |
| X60486 | H4 histone family; member G | Hs.46423 |
| AA132969 | metalloprotease 1 (pitrilysin family) | Hs.4812 |
| AA114250 | KIAA0512 gene product | Hs.48924 |
| F13782 | LIM binding domain 2 | Hs.4980 |
| AA283035 | ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | Hs.54813 |
| AB002301 | Human mRNA for KIAA0303 gene; partial cds | Hs.54985 |
| AA056731 | Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro) | Hs.554 |
| U68019 | MAD (mothers against decapentaplegic; Drosophila) homolog 3 | Hs.211578 |
| H99198 | ESTs; Moderately similar to THYMOSIN BETA-4 [H.sapiens] | Hs.56145 |
| AA598702 | bone morphogenetic protein 6 | Hs.6101 |
| N77151 | Homo sapiens mRNA for KIAA0799 protein; partial cds | Hs.61638 |
| AA505133 | ESTs | Hs.62273 |
| AB000584 | prostate differentiation factor | Hs.116577 |
| D12763 | interleukin 1 receptor-like 1 | Hs.66 |
| AA253193 | ESTs | Hs.6631 |
| AA432248 | ESTs | Hs.6738 |
| AA083572 | v-ral simian leukemia viral oncogene homolog A (ras related) | Hs.6906 |
| AA479713 | ESTs | Hs.71962 |
| L40395 | Homo sapiens clone 23689 mRNA; complete cds | Hs.170001 |
| X52947 | gap junction protein; alpha 1; 43kD (connexin 43) | Hs.74471 |
| W80846 | vesicle-associated membrane protein 5 (myobrevin) | Hs.74669 |
| M34539 | FK506-binding protein 1A (12kD) | Hs.752 |
| D67029 | SEC14 (S. cerevisiae)-like | Hs.75232 |
| U09587 | glycyl-tRNA synthetase | Hs.75280 |
| M85289 | Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds | Hs.211573 |
| D10522 | myristoylated alanine-rich protein kinase C substrate (MARCKS; 80K-L) | Hs.75607 |
| W84712 | calumenin | Hs.7753 |
| D29992 | tissue factor pathway inhibitor 2 | Hs.78045 |
| L34657 | platelet/endothelial cell adhesion molecule (CD31 antigen) | Hs.78146 |
| S78569 | laminin; alpha 4 | Hs.78672 |
| D43636 | Human mRNA for KIAA0096 gene; partial cds | Hs.79025 |
| U97188 | IGF-II mRNA-binding protein 3 | Hs.79440 |
| AA487558 | ESTs | Hs.8135 |
| M28882 | Human MUC18 glycoprotein mRNA, complete cds | Hs.211579 |
| X70683 | SRY (sex determining region Y)-box 4 | Hs.83484 |
| X14787 | thrombospondin 1 | Hs.87409 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA236324 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens] | Hs.92381 |
| C15324 | ESTs | Hs.93668 |
| AA452000 | ESTs | Hs.94030 |
| D83174 | collagen-binding protein 2 (colligen 2) | Hs.9930 |
| D00596 | Homo sapiens gene for thymidylate synthase; exons 1; 2; 3; 4; 5; 6; 7; complete cds | Hs.196351 |
| D11428 | peripheral myelin protein 22 | Hs.103724 |
| D13640 | major histocompatibility complex; class I; C | Hs.183618 |
| D14874 | adrenomedullin | Hs.394 |
| D26129 | ribonuclease; RNase A family; 1 (pancreatic) | Hs.78224 |
| D28476 | thyroid hormone receptor interactor 12 | Hs.138617 |
| D86425 | Homo sapiens mRNA for nidogen-2 | Hs.82733 |
| D86983 | Human mRNA for KIAA0230 gene; partial cds | Hs.118893 |
| D87953 | N-myc downstream regulated | Hs.75789 |
| HG1862-HT1897 | Calmodulin Type I | |
| HG2614-HT2710 | Collagen, Type Viii, Alpha 1 | |
| HG2639-HT2735 | Single-Stranded Dna-Binding Protein Mssp-1 | |
| HG2855-HT2995 | Heat Shock Protein, 70 Kda (Gb:Y00371) | |
| HG3044-HT3742 | Fibronectin, Alt. Splice 1 | |
| HG3342-HT3519 | Id1 | |
| HG3543-HT3739 | Insulin-Like Growth Factor 2 | |
| HG4069-HT4339 | Monocyte Chemotactic Protein 1 | |
| HG417-HT417 | Cathepsin B | |
| J03764 | plasminogen activator inhibitor; type I | Hs.82085 |
| L06797 | chemokine (C-X-C motif); receptor 4 (fusin) | Hs.89414 |
| L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | Hs.86386 |
| L12711 | transketolase (Wernicke-Korsakoff syndrome) | Hs.89643 |
| L13977 | prolylcarboxypeptidase (angiotensinase C) | Hs.75693 |
| L15388 | Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds | |
| L19871 | activating transcription factor 3 | Hs.460 |
| L20859 | Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds | Hs.78452 |
| L42176 | four and a half LIM domains 2 | Hs.8302 |
| L49169 | Human G0S3 mRNA; complete cds | Hs.75678 |
| L76380 | calcitonin receptor-like | Hs.152175 |
| M15990 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 | Hs.194148 |
| M23254 | calpain; large polypeptide L2 | Hs.76288 |
| M24736 | selectin E (endothelial adhesion molecule 1) | Hs.89546 |
| M26576 | collagen; type IV; alpha 1 | Hs.119129 |
| M27396 | asparagine synthetase | Hs.75692 |
| M31166 | pentaxin-related gene; rapidly induced by IL-1 beta | Hs.2050 |
| M31994 | Homo sapiens aldehyde dehydrogenase (ALDH1) gene, exon 13 and complete cds | |
| M32334 | intercellular adhesion molecule 2 | Hs.83733 |
| M35878 | insulin-like growth factor binding protein 3 | Hs.77326 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| M36429 | postmeiotic segregation increased 2-like 12 | Hs.89672 |
| M57730 | ephrin-A1 | Hs.1624 |
| M57731 | GRO2 oncogene | Hs.75765 |
| M60858 | nucleolin | Hs.79110 |
| M62994 | filamin B; beta (actin-binding protein-278) | Hs.81008 |
| M68874 | Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds | |
| M69043 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; alpha | Hs.81328 |
| M74719 | transcription factor 4 | Hs.75356 |
| M75126 | hexokinase 1 | Hs.118625 |
| M84349 | CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5; EJ16; EJ30; EL32 and G344) | Hs.119663 |
| M92843 | zinc finger protein homologous to Zfp-36 in mouse | Hs.198309 |
| M92934 | connective tissue growth factor | Hs.75511 |
| M93056 | protease inhibitor 2 (anti-elastase); monocyte/neutrophil | Hs.183583 |
| M94856 | fatty acid binding protein 5 (psoriasis-associated) | Hs.153179 |
| M95787 | transgelin | Hs.75777 |
| S76965 | Protein kinase inhibitor [human; neuroblastoma cell line SH-SY-5Y; mRNA; 2147 nt] | Hs.75209 |
| S81914 | DIFFERENTIATION-DEPENDENT GENE 2 | Hs.76095 |
| U03057 | singed (Drosophila)-like (sea urchin fascin homolog like) | Hs.118400 |
| U03100 | catenin (cadherin-associated protein); alpha 1 (102kD) | Hs.178452 |
| U03877 | EGF-containing fibulin-like extracellular matrix protein 1 | Hs.76224 |
| U08021 | nicotinamide N-methyltransferase | Hs.76669 |
| U14391 | myosin IC | Hs.82251 |
| U31384 | guanine nucleotide binding protein 11 | Hs.83381 |
| U32944 | dynein; cytoplasmic; light polypeptide | Hs.5120 |
| U40369 | Human spermidine/spermine N1-acetyltransferase (SSAT) gene, complete cds | |
| U41767 | Human metargidin precursor mRNA, complete cds | |
| U48959 | Homo sapiens myosin light chain kinase (MLCK) mRNA; complete cds | Hs.75950 |
| U51010 | Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region | |
| U51478 | ATPase; Na+/K+ transporting; beta 3 polypeptide | Hs.76941 |
| U53445 | Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA; complete cds | Hs.15432 |
| U59289 | cadherin 13; H-cadherin (heart) | Hs.63984 |
| U59423 | MAD (mothers against decapentaplegic; Drosophila) homolog 1 | Hs.79067 |
| U62015 | Homo sapiens Cyr61 mRNA, complete cds | |
| U63825 | Human hepatitis delta antigen interacting protein A (dipA) mRNA; complete cds | Hs.66713 |
| U67963 | Human lysophospholipase homolog (HU-K5) mRNA; complete cds | Hs.6721 |
| U73379 | Human cyclin-selective ubiquitin carrier protein mRNA; complete cds | Hs.93002 |
| U73824 | eukaryotic translation initiation factor 4 gamma; 2 | Hs.183684 |
| U77604 | microsomal glutathione S-transferase 2 | Hs.81874 |
| U81607 | kinase scaffold protein gravin | Hs.788 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| U89942 | lysyl oxidase-like 2 | Hs.83354 |
| X04412 | gelsolin (amyloidosis; Finnish type) | Hs.80562 |
| X06985 | heme oxygenase (decycling) 1 | Hs.75967 |
| X07820 | matrix metalloproteinase 10 (stromelysin 2) | Hs.2258 |
| X12876 | keratin 18 | Hs.65114 |
| X15729 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase; 68kD) | Hs.76053 |
| X52541 | early growth response 1 | Hs.738 |
| X53416 | filamin A; alpha (actin-binding protein-280) | Hs.76279 |
| X54489 | GRO1 oncogene (melanoma growth stimulating activity; alpha) | Hs.789 |
| X54925 | matrix metalloproteinase 1 (interstitial collagenase) | Hs.83169 |
| X57206 | inositol 1;4;5-trisphosphate 3-kinase B | Hs.78877 |
| X59798 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | Hs.82932 |
| X60957 | tyrosine kinase with immunoglobulin and epidermal growth factor homology domains | Hs.78824 |
| X65965 | H.sapiens SOD-2 gene for manganese superoxide dismutase | |
| X69111 | inhibitor of DNA binding 3; dominant negative helix-loop-helix protein | Hs.76884 |
| X70940 | eukaryotic translation elongation factor 1 alpha 2 | Hs.2642 |
| X87838 | catenin (cadherin-associated protein); beta 1 (88kD) | Hs.171271 |
| X91247 | thioredoxin reductase 1 | Hs.13046 |
| X97748 | H.sapiens PTX3 gene promotor region | |
| Y00815 | protein tyrosine phosphatase; receptor type; F | Hs.75216 |
| AA303711 | ephrin-B1 | Hs.144700 |
| L44538 | ESTs | Hs.156044 |
| AA025351 | ESTs | Hs.134797 |
| AA027050 | ESTs | Hs.31189 |
| AA029462 | ESTs | Hs.17235 |
| AA045136 | ESTs | Hs.22575 |
| AA047437 | ESTs | Hs.22968 |
| AA054087 | phospholipase A2; group IVC (cytosolic; calcium-independent) | Hs.18858 |
| AA071089 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] | Hs.187932 |
| AA156450 | ESTs; Weakly similar to Similar to Rat trg gene product [C.elegans] | Hs.8982 |
| AA187490 | ESTs | Hs.21941 |
| AA195031 | ESTs; Moderately similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [H.sapiens] | Hs.9305 |
| AA205724 | ESTs | Hs.10119 |
| AA227926 | ESTs | Hs.6682 |
| AA227986 | ESTs | Hs.25329 |
| AA234743 | ESTs | Hs.22120 |
| AA253216 | ESTs | Hs.22283 |
| AA256210 | oncomodulin | Hs.199134 |
| AA256268 | ESTs | Hs.10283 |
| AA279397 | ESTs; Moderately similar to fibronectin [H.sapiens] | Hs.25001 |
| AA292379 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | Hs.20340 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA292717 | ESTs; Weakly similar to JM2 [H.sapiens] | Hs.7891 |
| AA346551 | ESTs | Hs.23457 |
| AA400292 | ESTs | Hs.23786 |
| AA404338 | ESTs | Hs.21812 |
| AA412284 | poliovirus receptor | Hs.171844 |
| AA423987 | ESTs | Hs.7567 |
| AA428594 | ESTs | Hs.21321 |
| AA430108 | ESTs | Hs.6019 |
| AA431462 | ESTs | Hs.28329 |
| AA431470 | ESTs; Weakly similar to CAMP-DEPENDENT PROTEIN KINASE INHIBITOR; MUSCLE/BRAIN FORM [H.sapiens] | Hs.3407 |
| AA443756 | ESTs; Moderately similar to (defline not available 4105275) [H.sapiens] | Hs.6673 |
| AA449479 | ESTs; Highly similar to (defline not available 5106787) [H.sapiens] | Hs.5216 |
| AA459916 | bradykinin receptor B2 | Hs.25021 |
| AA465226 | ESTs | Hs.28631 |
| AA478778 | ESTs | Hs.16450 |
| AA479037 | ESTs | Hs.7961 |
| AA482597 | ESTs; Highly similar to (defline not available 4704739) [H.sapiens] | Hs.26054 |
| AA487561 | ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1A [H.sapiens] | Hs.9813 |
| AA489245 | ESTs; Weakly similar to sperm specific protein [H.sapiens] | Hs.5682 |
| AA504110 | ESTs | Hs.18063 |
| AA520989 | ESTs; Highly similar to SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT [H.sapiens] | Hs.9195 |
| AA599434 | ESTs | Hs.25035 |
| AA608649 | Homo sapiens clone 23742 mRNA; partial cds | Hs.6354 |
| AA609519 | ESTs | Hs.26458 |
| D51069 | Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds | Hs.185718 |
| U97519 | podocalyxin-like | Hs.16426 |
| W28391 | proliferation-associated 2G4; 38kD | Hs.5181 |
| AA035638 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053) | Hs.71968 |
| AA083514 | ESTs | Hs.68301 |
| AA121315 | ESTs | Hs.70823 |
| AA147186 | ESTs | Hs.92387 |
| AA156125 | ESTs | Hs.72116 |
| AA188932 | ESTs | Hs.85640 |
| AA219653 | ESTs | Hs.87125 |
| AA232645 | ESTs | Hs.42699 |
| F10078 | ESTs | Hs.13233 |
| H48032 | ESTs | Hs.9645 |
| H82117 | ESTs | Hs.28043 |
| N39584 | ESTs | Hs.17404 |
| N54067 | Homo sapiens mRNA for NIK; partial cds | Hs.3628 |
| N59858 | ESTs | Hs.33032 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| N90933 | ESTs | Hs.4867 |
| N93764 | ESTs; Moderately similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens] | Hs.10175 |
| R26124 | ESTs | Hs.24024 |
| R27957 | ESTs | Hs.24230 |
| R55470 | ESTs; Moderately similar to K02E10.2 [C.elegans] | Hs.11067 |
| T16550 | ESTs; Highly similar to vacuolar protein sorting homolog h-vps45 [H.sapiens] | Hs.6650 |
| T26674 | ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens] | Hs.6966 |
| T57112 | yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence. | Hs.8881 |
| T88700 | ESTs | Hs.173374 |
| T90527 | ESTs | Hs.7890 |
| W42789 | ESTs | Hs.31446 |
| W60002 | plastin 3 (T isoform) | Hs.4114 |
| W78175 | ESTs | Hs.17901 |
| W84768 | ESTs | Hs.141742 |
| W94427 | ESTs; Weakly similar to Na;K-ATPase gamma subunit [H.sapiens] | Hs.3807 |
| AA253217 | ESTs | Hs.41271 |
| AA426573 | ESTs | Hs.41135 |
| AA432374 | ESTs | Hs.48029 |
| AA446622 | ESTs | Hs.74313 |
| AA478771 | ESTs | Hs.50841 |
| AA482594 | ESTs | Hs.62684 |
| AA490588 | ESTs | Hs.43118 |
| D59570 | ESTs | Hs.17132 |
| H88157 | ESTs | Hs.41105 |
| H94648 | ESTs | Hs.41995 |
| H97538 | ESTs | Hs.42392 |
| H98670 | ESTs; Weakly similar to (defline not available 4884081) [H.sapiens] | Hs.49753 |
| N22107 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens] | Hs.172241 |
| W38197 | Accession not listed in Genbank | |
| W80814 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens] | Hs.196785 |
| AA287347 | ESTs | Hs.105088 |
| AA402799 | ESTs | Hs.182538 |
| AA404418 | EST | Hs.144953 |
| AA425107 | ESTs | Hs.97016 |
| AA425435 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | Hs.98438 |
| AA442872 | ESTs | Hs.110771 |
| AA452860 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens] | Hs.197214 |
| AA488687 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | Hs.190307 |
| AA599674 | ESTs; Weakly similar to ORF [D.melanogaster] | Hs.108115 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| F13673 | ESTs | Hs.99769 |
| H99093 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72kD) | Hs.6179 |
| N22495 | yw35g11.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:254276 3', mRNA sequence. | Hs.102415 |
| N23031 | myosin; heavy polypeptide 7; cardiac muscle; beta | Hs.929 |
| R15740 | carbohydrate (chondroitin 6/keratan) sulfotransferase 1 | Hs.104576 |
| R39610 | calpain; large polypeptide L2 | Hs.76288 |
| W45560 | ESTs | Hs.102541 |
| Z39833 | H.sapiens mRNA for Rho6 protein | Hs.124940 |
| Z40583 | ESTs | Hs.101259 |
| AA825437 | ESTs | |
| R66613 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053) | |
| AA868063 | carbohydrate (chondroitin 6/keratan) sulfotransferase 1 | |
| AA128075 | zl16d08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:502095 5', mRNA sequence. | |
| N66570 | ESTs | |
| AI051390 | ESTs | |
| AA627122 | ESTs | |
| X02761 | fibronectin 1 | Hs.118162 |
| AF010193 | MAD (mothers against decapentaplegic; Drosophila) homolog 7 | Hs.100602 |
| AA149044 | ESTs; Highly similar to the KIAA0195 gene is expressed ubiquitously. [H.sapiens] | Hs.10086 |
| U82108 | solute carrier family 9 (sodium/hydrogen exchanger); isoform 3 regulatory factor 2 | Hs.101813 |
| D78676 | ESTs; Moderately similar to (defline not available 4529890) [H.sapiens] | Hs.105509 |
| L35240 | enigma (LIM domain protein) | Hs.102948 |
| AA598737 | lactate dehydrogenase B | Hs.180414 |
| R69417 | ESTs | Hs.107055 |
| AA232837 | ESTs; Weakly similar to Human pre-mRNA cleavage factor I 68 kDa subunit [H.sapiens] | Hs.107125 |
| N72695 | ESTs | Hs.108557 |
| M30257 | vascular cell adhesion molecule 1 | Hs.109225 |
| M96843 | inhibitor of DNA binding 2; dominant negative helix-loop-helix protein | Hs.109617 |
| X68277 | dual specificity phosphatase 1 | Hs.171695 |
| AA292440 | myeloid differentiation primary response | Hs.110571 |
| J03040 | secreted protein; acidic; cysteine-rich (osteonectin) | Hs.111779 |
| AA228107 | ESTs | Hs.54642 |
| AA449789 | connective tissue growth factor | Hs.75511 |
| W01367 | ESTs | Hs.170980 |
| AA610116 | ESTs; Highly similar to (defline not available 4325180) [H.sapiens] | Hs.11663 |
| AA258308 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053) | Hs.165618 |
| AA460273 | Homo sapiens mRNA for KIAA0517 protein; partial cds | Hs.12372 |
| AA286710 | lymphocyte adaptor protein | Hs.13131 |
| T68873 | metallothionein 1L | Hs.143289 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| D63476 | PAK-interacting exchange factor beta | Hs.172813 |
| M62403 | insulin-like growth factor-binding protein 4 | Hs.1516 |
| X55740 | 5' nucleotidase (CD73) | Hs.153952 |
| L10284 | calnexin | Hs.155560 |
| AA243278 | ribosomal protein; mitochondrial; L12 | Hs.109059 |
| AA430032 | pituitary tumor-transforming 1 | Hs.159626 |
| H16402 | ESTs | Hs.17121 |
| D59711 | ESTs | Hs.17132 |
| T94452 | ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence | |
| AA431571 | ESTs | Hs.17894 |
| R79356 | Homo sapiens mRNA for KIAA0544 protein; partial cds | Hs.19280 |
| AA280375 | ESTs | Hs.19928 |
| Z49269 | small inducible cytokine subfamily A (Cys-Cys); member 14 | Hs.20144 |
| Z41740 | ESTs | Hs.24462 |
| AA121543 | Homo sapiens mRNA for KIAA0758 protein; partial cds | Hs.22039 |
| J05008 | endothelin 1 | Hs.2271 |
| AA101878 | ESTs | Hs.22793 |
| T35341 | ESTs; Highly similar to (defline not available 4519883) [H.sapiens] | Hs.22880 |
| N87590 | ESTs | Hs.23037 |
| AA256153 | ESTs | Hs.23912 |
| W74533 | Homo sapiens mRNA for KIAA0786 protein; partial cds | Hs.24212 |
| U25997 | stanniocalcin | Hs.25590 |
| V01512 | v-fos FBJ murine osteosarcoma viral oncogene homolog | Hs.25647 |
| X56681 | jun D proto-oncogene | Hs.2780 |
| AA161292 | interferon; alpha-inducible protein 27 | Hs.2867 |
| AA491465 | ESTs | Hs.28792 |
| AA046593 | ESTs | Hs.28959 |
| D50914 | Human mRNA for KIAA0124 gene; partial cds | Hs.30736 |
| D45304 | ESTs | Hs.31595 |
| M90657 | transmembrane 4 superfamily member 1 | Hs.3337 |
| W69127 | ESTs; Weakly similar to zinc finger protein ZNF191 [H.sapiens] | Hs.3449 |
| AA316186 | ESTs; Highly similar to (defline not available 4262136) [H.sapiens] | Hs.34549 |
| AA384503 | ESTs | Hs.179260 |
| AA136353 | ESTs | Hs.38022 |
| AA044755 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] | Hs.173705 |
| U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 | Hs.41270 |
| AA058911 | ESTs; Weakly similar to membrane glycoprotein [M.musculus] | Hs.4193 |
| AA620962 | dynein; cytoplasmic; light intermediate polypeptide 2 | Hs.44251 |
| AA285290 | small EDRK-rich factor 2 | Hs.44499 |
| X60486 | H4 histone family; member G | Hs.46423 |
| R31641 | ESTs | Hs.197148 |
| AA489190 | ESTs | Hs.48320 |
| F13782 | LIM binding domain 2 | Hs.4980 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| AA257993 | Janus kinase 1 (a protein tyrosine kinase) | Hs.50651 |
| M24283 | intercellular adhesion molecule 1 (CD54); human rhinovirus receptor | Hs.168383 |
| AA443114 | ESTs; Weakly similar to PIM-1 PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE [H.sapiens] | Hs.5326 |
| T35289 | casein kinase 1; alpha 1 | Hs.195206 |
| N23817 | Homo sapiens clone 23675 mRNA sequence | Hs.5807 |
| AA047151 | ESTs | Hs.5897 |
| N77151 | Homo sapiens mRNA for KIAA0799 protein; partial cds | Hs.61638 |
| AA480074 | ESTs | Hs.62206 |
| Y00787 | interleukin 8 | Hs.624 |
| T99789 | ESTs | Hs.64313 |
| W84341 | tissue inhibitor of metalloproteinase 2 | Hs.6441 |
| L09209 | amyloid beta (A4) precursor-like protein 2 | Hs.64797 |
| D12763 | interleukin 1 receptor-like 1 | Hs.66 |
| T16484 | ESTs | Hs.6607 |
| AA253193 | ESTs | Hs.6631 |
| AA432248 | ESTs | Hs.6738 |
| X82200 | stimulated trans-acting factor (50 kDa) | Hs.68054 |
| AA083572 | v-ral simian leukemia viral oncogene homolog A (ras related) | Hs.6906 |
| L00352 | low density lipoprotein receptor (familial hypercholesterolemia) | Hs.181182 |
| N75791 | ESTs | Hs.7153 |
| X57579 | H.sapiens activin beta-A subunit (exon 2) | |
| X02612 | cytochrome P450; subfamily I (aromatic compound-inducible); polypeptide 1 | Hs.72912 |
| H44631 | immediate early protein | Hs.737 |
| AA090257 | superoxide dismutase 2; mitochondrial | Hs.177781 |
| X83703 | H.sapiens mRNA for cytokine inducible nuclear protein | Hs.74019 |
| L40395 | Homo sapiens clone 23689 mRNA; complete cds | Hs.170001 |
| AA227913 | ESTs | Hs.198456 |
| X52947 | gap junction protein; alpha 1; 43kD (connexin 43) | Hs.74471 |
| M11313 | alpha-2-macroglobulin | Hs.74561 |
| L14837 | tight junction protein 1 (zona occludens 1) | Hs.74614 |
| M60721 | Human homeobox gene, complete cds | |
| D90209 | activating transcription factor 4 (tax-responsive enhancer element B67) | Hs.181243 |
| T67986 | yc28e12.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82030 3' similar to gb:X14723 CLUSTERIN PRECURSOR | Hs.75106 |
| AA148318 | Human mRNA for KIAA0069 gene; partial cds | Hs.75249 |
| U97105 | dihydropyrimidinase-like 2 | Hs.173381 |
| T25747 | H.sapiens OZF mRNA | Hs.75471 |
| K02574 | Accession not listed in Genbank | |
| D78577 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; eta polypeptide | Hs.75544 |
| X53331 | matrix Gla protein | Hs.75742 |
| S73591 | upregulated by 1;25-dihydroxyvitamin D-3 | Hs.179526 |
| X95735 | zyxin | Hs.75873 |

| Exemplar Accession | Complete Title | UniGeneID(11/29/99) |
|---|---|---|
| L16862 | G protein-coupled receptor kinase 6 | Hs.76297 |
| U44975 | Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA; complete cds | Hs.76526 |
| M97796 | inhibitor of DNA binding 2; dominant negative helix-loop-helix protein | Hs.180919 |
| U86782 | 26S proteasome-associated pad1 homolog | Hs.178761 |
| AA099391 | ESTs | Hs.77310 |
| M19267 | tropomyosin 1 (alpha) | Hs.77899 |
| D29992 | tissue factor pathway inhibitor 2 | Hs.78045 |
| L19314 | phosphorylase kinase; beta | Hs.195217 |
| S78569 | laminin; alpha 4 | Hs.78672 |
| U28811 | Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA, complete cds | |
| L77886 | protein tyrosine phosphatase; receptor type; K | Hs.79005 |
| C14407 | neuronal tissue-enriched acidic protein | Hs.79516 |
| M60278 | diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) | Hs.799 |
| R81509 | splicing factor; arginine/serine-rich 11 | Hs.184571 |
| AA487558 | ESTs | Hs.8135 |
| D86962 | KIAA0207 gene product | Hs.81875 |
| AA478971 | disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein) | Hs.81988 |
| D50683 | transforming growth factor; beta receptor II (70-80kD) | Hs.82028 |
| U56637 | capping protein (actin filament) muscle Z-line; alpha 1 | Hs.184270 |
| M61199 | Human cleavage signal 1 protein mRNA; complete cds | Hs.82767 |
| M28882 | Human MUC18 glycoprotein mRNA, complete cds | |
| X15183 | CDW52 antigen (CAMPATH-1 antigen) | Hs.180532 |
| S53911 | CD34 | Hs.85289 |
| U20734 | Human transcription factor junB (junB) gene; 5' region and complete cds | Hs.198951 |
| D28235 | prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) | Hs.92309 |
| AA236324 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens] | Hs.92381 |
| AA148923 | Homo sapiens mRNA for DEPP (decidual protein induced by progesterone); complete cds | Hs.93675 |
| AA174183 | ESTs | Hs.93872 |
| AA456311 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens] | Hs.93961 |
| L08069 | heat shock protein; DNAJ-like 2 | Hs.94 |
| AA452000 | ESTs | Hs.94030 |
| AA282140 | ESTs | Hs.9587 |
| J02854 | myosin regulatory light chain 2; smooth muscle isoform | Hs.9615 |
| AA442054 | phospholipase C; gamma 1 (formerly subtype 148) | Hs.993 |

TABLE 5

| Accession # | UniGeneID | Title | Gene | Eos # |
|---|---|---|---|---|
| AA426573 | Hs.41135 | ESTs; Moderately similar to endomucin [M.musculus] | | AAA9 |
| D58024 | Hs.57958 | ESTs; Weakly similar to KIAA0768 protein [H.sapiens] | | AAA8 |
| M31210 | Hs.154210 | endothelial differentiation; sphingolipid G-protein-coupled receptor; 1 | EDG1 | AAA7 |
| X06256 | Hs.149609 | integrin; alpha 5 (fibronectin receptor; alpha polypeptide) | ITGA5 | AAB1 |
| L20859 | Hs.78452 | solute carrier family 20 (phosphate transporter); member 1 | SLC20A1 | AAB3 |
| X07820 | Hs.2258 | matrix metalloproteinase 10 (stromelysin 2) | MMP10 | AAB4 |
| AA234743 | Hs.22120 | ESTs | | AAB5 |
| U97519 | Hs.16426 | podocalyxin-like | PODXL | AAB6 |
| U03877 | Hs.76224 | EGF-containing fibulin-like extracellular matrix protein 1 | EFEMP1 | AAB8 |
| M28882 | Hs.211579 | melanoma adhesion molecule | MCAM | AAB9 |
| X54925 | Hs.83169 | matrix metalloproteinase 1 (interstitial collagenase) | MMP1 | AAC1 |
| AA045136 | Hs.22575 | ESTs | | AAC2 |
| AA423987 | Hs.7567 | ESTs | | AAC3 |
| AA234743 | Hs.22120 | ESTs | | AAC4 |
| AA156125 | Hs.72116 | ESTs; Moderately similar to hedgehog-interacting protein [M.musculus] | | AAC5 |
| AA025351 | Hs.134797 | ESTs | | AAC6 |
| AA432248 | Hs.6738 | ESTs | | AAC7 |
| AA227926 | Hs.6682 | ESTs | | AAC8 |
| AA187490 | Hs.21941 | ESTs | | AAD1 |
| AA232645 | Hs.42699 | ESTs | | AAD2 |

CLAIMS

We claim:

1. A method of screening drug candidates comprising:
   a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5 or a fragment thereof;
   b) adding a drug candidate to said cell; and
   c) determining the effect of said drug candidate on the expression of said expression profile gene.

2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.

3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.

4. A method of screening for a bioactive agent capable of binding to a angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5, or a fragment thereof, said method comprising combining said AMP and a candidate bioactive agent, and determining the binding of said candidate agent to said AMP.

5. A method for screening for a bioactive agent capable of modulating the activity of a angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5, or a fragment thereof, said method comprising:
   a) combining said AMP and a candidate bioactive agent; and
   b) determining the effect of said candidate agent on the bioactivity of said AMP.

6. A method of evaluating the effect of a candidate angiogenesis drug comprising:
   a) administering said drug to a patient;
   b) removing a cell sample from said patient; and
   c) determining the expression profile of said cell.

7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A method of diagnosing angiogenesis comprising:

a) determining the expression of one or more genes selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5, or a fragment thereof in a first tyupe of a first individual; and

b) comparing said expression of said gene(s) from a second normal tissue type from said first individual or a second unaffected individual, wherein a difference in said expression indicates that the first individual has tissue that is undergoing angiogenesis.

9. A biochip comprising a nucleic acid segment selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3, Table 4 and Table 5, wherein said biochip comprises fewer than 1000 nucleic acid probes.

10. A biochip according to claim 9 comprising at least two nucleic acid segments.

11. A method for screening for a bioactive agent capable of interfering with the binding of an angiogenesis modulator protein (AMP) or a fragment thereof and an antibody which binds to said AMP or fragment thereof, said method comprising:

a) combining anAMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said AMP or fragment thereof; and

b) determining the binding of said AMP or fragment thereof and said antibody.

12. A method for inhibiting the activity of an angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5 or a fragment thereof, said method comprising binding an inhibitor to said AMP.

13. A method according to claim 12 wherein said inhibitor is an antibody.

14. A method of treating a disorder associated with angiogenesis comprising administering to a patient an inhibitor of n angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5 or a fragment thereof.

15. A method according to claim 14 wherein said inhibitor is an antibody.

16. A method of neutralizing the effect of an AMP, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

17. A method for localizing a therapeutic moiety to angloggenic tissue comprising exposing said tissue to an antibody to an AMP or fragment thereof conjugated to said therapeutic moiety.

18. The method of Claim 17, wherein said therapeutic moiety is a cytotoxic agent.

19. The method of Claim 17, wherein said therapeutic moiety is a radioisotope.

20. A method for inhibiting angiogenesis in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5.

21. An antibody which specifically binds to a protein encoded by a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or a fragment thereof.

22. The antibody of Claim 21, wherein said antibody is a monoclonal antibody.

23. The antibody of Claim 21, wherein said antibody is a humanized antibody.

24. The antibody of Claim 21, wherein said antibody is an antibody fragment.

25. A nucleic acid having a sequence at least 95% homologous to a sequence of a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or its complement.

26. A nucleic acid which hybridizes under high stringency to a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or its complement.

27. A polypeptide encoded by the nucleic acid of Claim 25 or 26.

28. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising the polypeptide of Claim 27 or a fragment thereof.

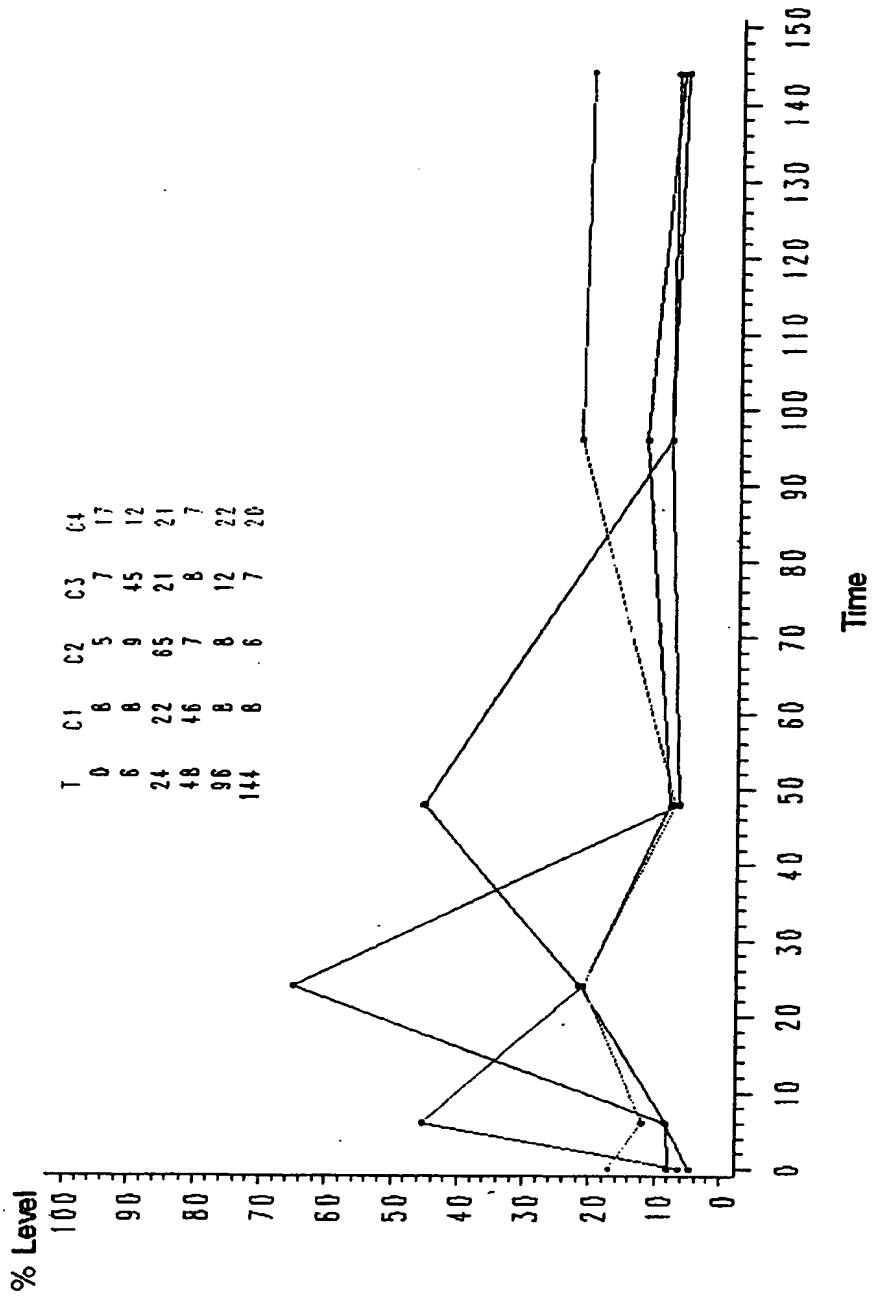
29. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence of a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or a fragment thereof.

30. A method for determining the prognosis of an individual with a disorder associated with angiogenesis comprising determining the level of a AMP in a sample, wherein a high level of the AMP indicates a poor prognosis.

31. A method of treating a disorder associated with angiogenisis comprising administering to an individual having a disorder associated with angiogenesis an antibody to a AMP or fragment thereof conjugated to a therapeutic moiety.

32. The method of Claim 31, wherein said therapeutic moiety is a cytotoxic agent.

33. The method of Claim 31, wherein said therapeutic moiety is a radioisotope.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No Map Present: PNull < 0.000005
T C1 C2 C3 C4
0 8 5 7 17
6 8 9 45 12
24 22 65 21 21
48 46 7 8 7
96 8 8 12 22
144 8 6 7 20
% Level
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70
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50
40
30
20
10
0
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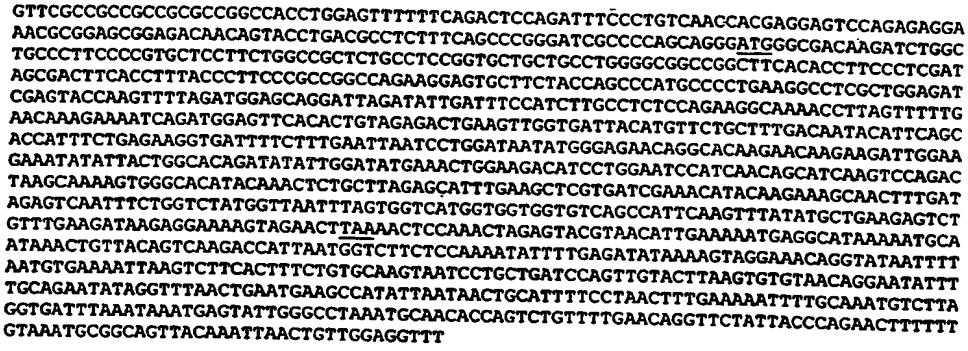
Time

FIGURE 1

FIGURE 2



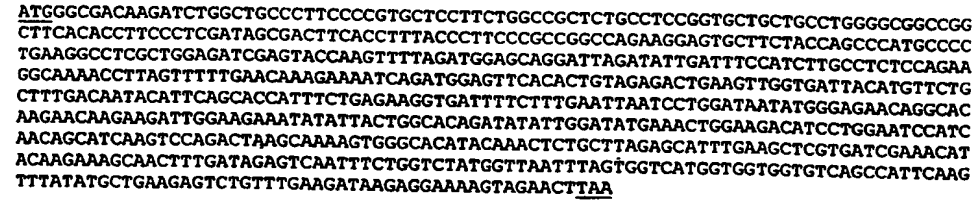




FIGURE 3

# FIGURE 4

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEYQVLDGAGL
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KYITGTDILDMKLEDILESINSIKSRLSKSGHIQTLLRAFEARDRNIQESNFDRVNFWSMVNLVVMVVVS
AIQVYMLKSLFEDKRKSRT.

# FIGURE 5

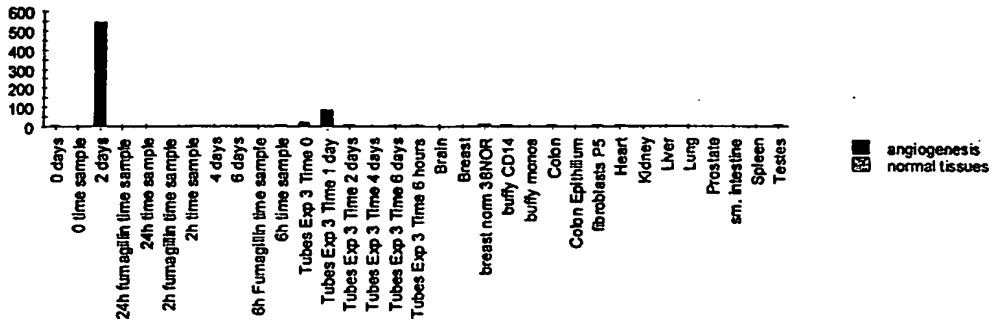
Peptide Name: AAA4p1

Sequence: H-Cys-Met-Leu-Lys-Ser-Leu-Phe-Glu-Asp-Lys
-Arg-Lys-Ser-Arg-Thr-OH

Peptide Name: AAA4p2

Sequence: H-Cys-Ala-Gly-Phe-Thr-Pro-Ser-Leu-Asp-Ser-Asp
-Phe-Thr-Phe-Thr-$NH_2$

FIGURE 6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500
400
300
200
100
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0 days
0 time sample
2 days
24h fumagillin time sample
24h time sample
2h fumagillin time sample
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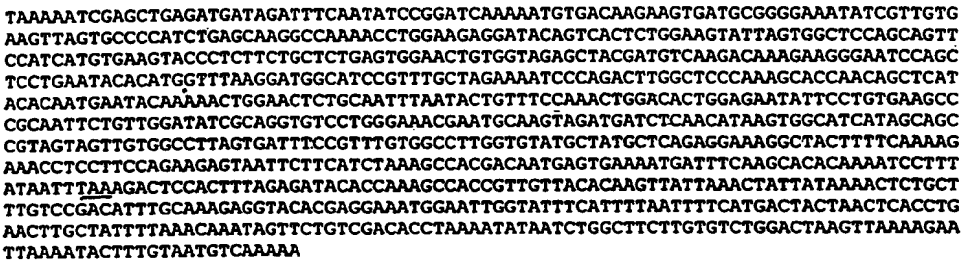
4 days
6 days
6h Fumagillin time sample
6h time sample
Tubes Exp 3 Time 0
Tubes Exp 3 Time 1 day
Tubes Exp 3 Time 2 days
Tubes Exp 3 Time 4 days
Tubes Exp 3 Time 6 days
Tubes Exp 3 Time 6 hours
Brain
Breast
breast norm 38NOR
buffy CD14
buffy mono
Colon
Colon Epithilium
fibroblasts P5
Heart
Kidney
Liver
Lung
Prostate
sm. intestine
Spleen
Testes
angiogenesis
normal tissues

FIGURE 7



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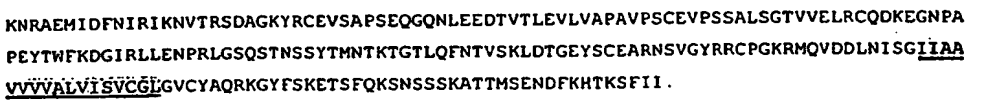

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VVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII.

FIGURE 8

# FIGURE 9

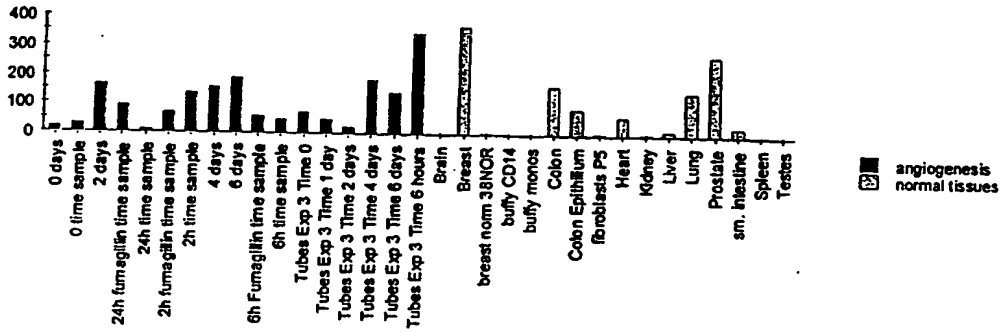
Peptide Name: AAA1p1

Sequence: H-Cys-Ala-Thr-Thr-Met-Ser-Glu-Asn-Asp-Phe-Lys-His-Thr-Lys-Ser-$NH_2$

Peptide Name: AAA1p2

Sequence: Ac-Arg-Cys-Gln-Asp-Lys-Glu-Gly-Asn-Pro-Ala-Pro-Glu-Tyr-Thr-$NH_2$

FIGURE 10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200
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0 time sample
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24h time sample
2h fumagillin time sample
2h time sample
4 days
6 days
6h Fumagillin time sample
6h time sample
Tubes Exp 3 Time 0
Tubes Exp 3 Time 1 day
Tubes Exp 3 Time 2 days
Tubes Exp 3 Time 4 days
Tubes Exp 3 Time 6 days
Tubes Exp 3 Time 6 hours
Brain
Breast
breast norm 38NOR
buffy CD14
buffy monos
Colon
Colon Epithelium
fibroblasts P5
Heart
Kidney
Liver
Lung
Prostate
sm. intestine
Spleen
Testes
angiogenesis
normal tissues

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FIGURE 11

FIGURE 12

ATGGGGCCCACCAGCGTCCCGCTGGTCAAGGCCCACCGCAGCTCGGTCTCTGACTACGTCAACTATGATATCATCGTCCG
GCATTACAACTACACGGGAAAGCTGAATATCAGCGCGGACAAGGAGAACAGCATTAAACTGACCTCGGTGGTGTTCATTC
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CTGGAAACGTCAACTCTTCTTCCTAG

FIGURE 13

MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISADKENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLKMKLHNGSNNFRI
FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHKHYILFCTTVFTLLLLSIVILYCRIYSLVRTRSRRLTFRKN
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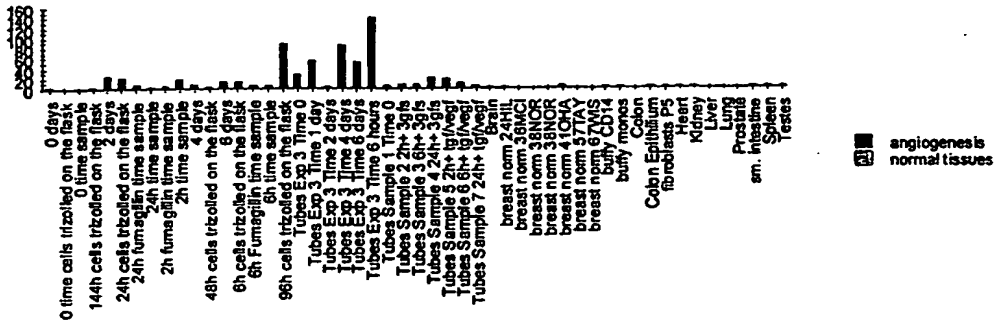
FIRIMSCCKCPSGDSAGKFKRPIIAGMEFSRSKSDNSSHPQKDEGDNPETIMSSGNVNSSS.

# FIGURE 14

| Peptide names | amino acid sequence | Solubility |
|---|---|---|
| AAA7p1 | Ac-KLNISADKENSIKLC-NH2 | 1mg/1ml H2O |
| AAA7p2 | H-CTTYKLTPAQWFLRE-NH2 | min.amt.DMSO/H2O |
| AAA7p3 | H-CNPIIYTLTNKEMRR-NH2 | 1mg/1ml H2O |
| AAA7p1m | Ac-KLNIGAEKDHGIKLC-NH2 | 1mg/1ml H2O |

FIGURE 15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0 time sample
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24h fumagillin time sample
24h time sample
2h fumagillin time sample
2h time sample
4 days
48h cells trizolled on the flask
8 days
6h cells trizolled on the flask
6h Fumagillin time sample
6h time sample
96h cells trizolled on the flask
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Tubes Exp 3 Time 2 days
Tubes Exp 3 Time 4 days
Tubes Exp 3 Time 6 days
Tubes Exp 3 Time 6 hours
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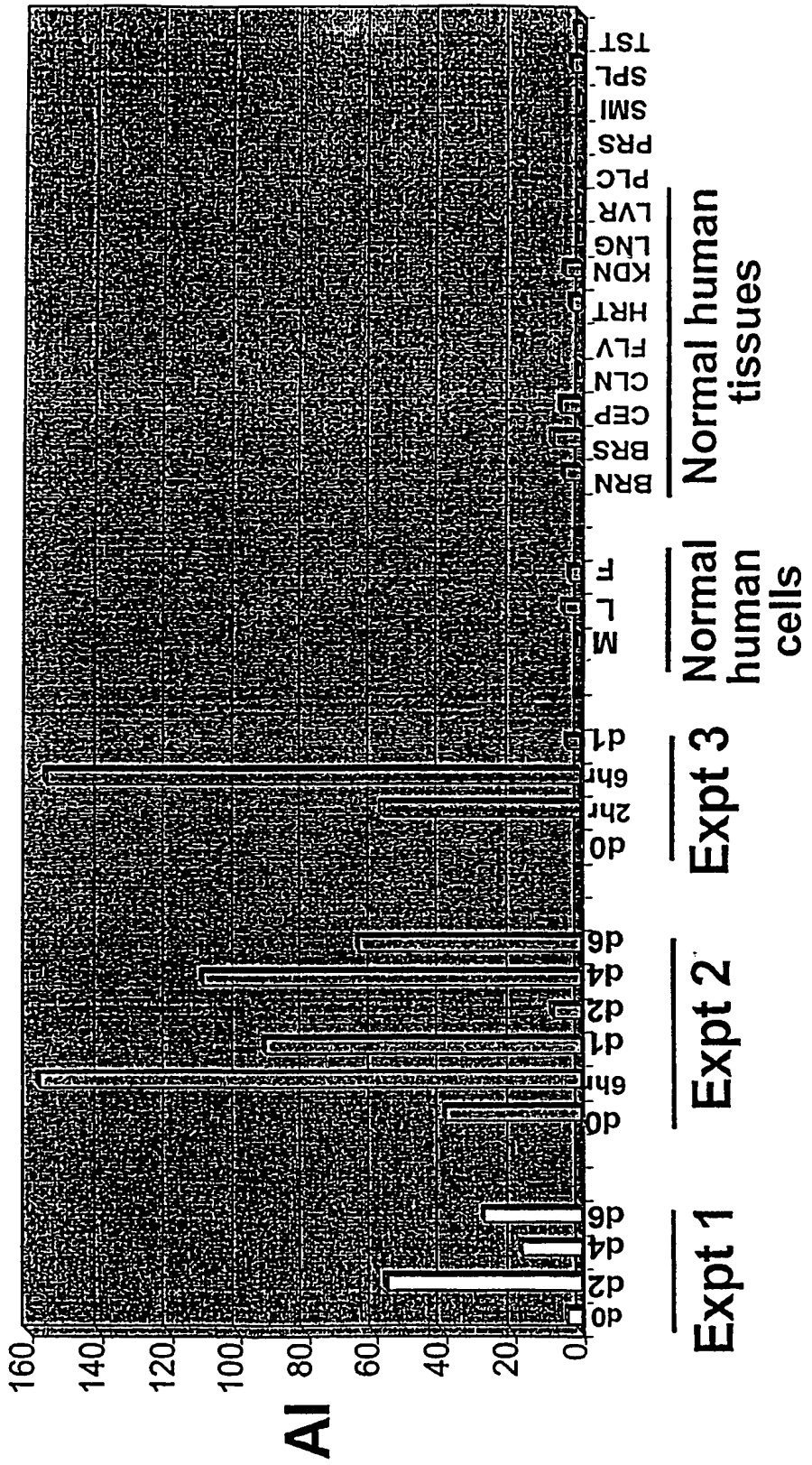
Tubes Sample 3 6h+ 3gfs
Tubes Sample 4 24h+ 3gfs
Tubes Sample 5 2h+ tg/Vegf
Tubes Sample 6 6h+ tg/Vegf
Tubes Sample 7 24h+ tg/Vegf
Brain
breast norm 24HIL
breast norm 36MCI
breast norm 38NOR
breast norm 38NOR
breast norm 41OHA
breast norm 57TAY
breast norm 67WIS
buffy CD14
buffy monos
Colon
Colon Epithelium
fibroblasts P5
Heart
Kidney
Liver
Lung
Prostate
sm. intestine
Spleen
Testes
angiogenesis
normal tissues

FIGURE 16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6hr
d1
d2
d4
d6
d0
2hr
6hr
d1
M
L
F
BRN
BRS
CEP
CLN
FLV
HRT
KDN
LNG
LVR
PLC
PRS
SMI
SPL
TST
Expt 1
Expt 2
Expt 3
Normal human cells
Normal human tissues

# FIGURE 17

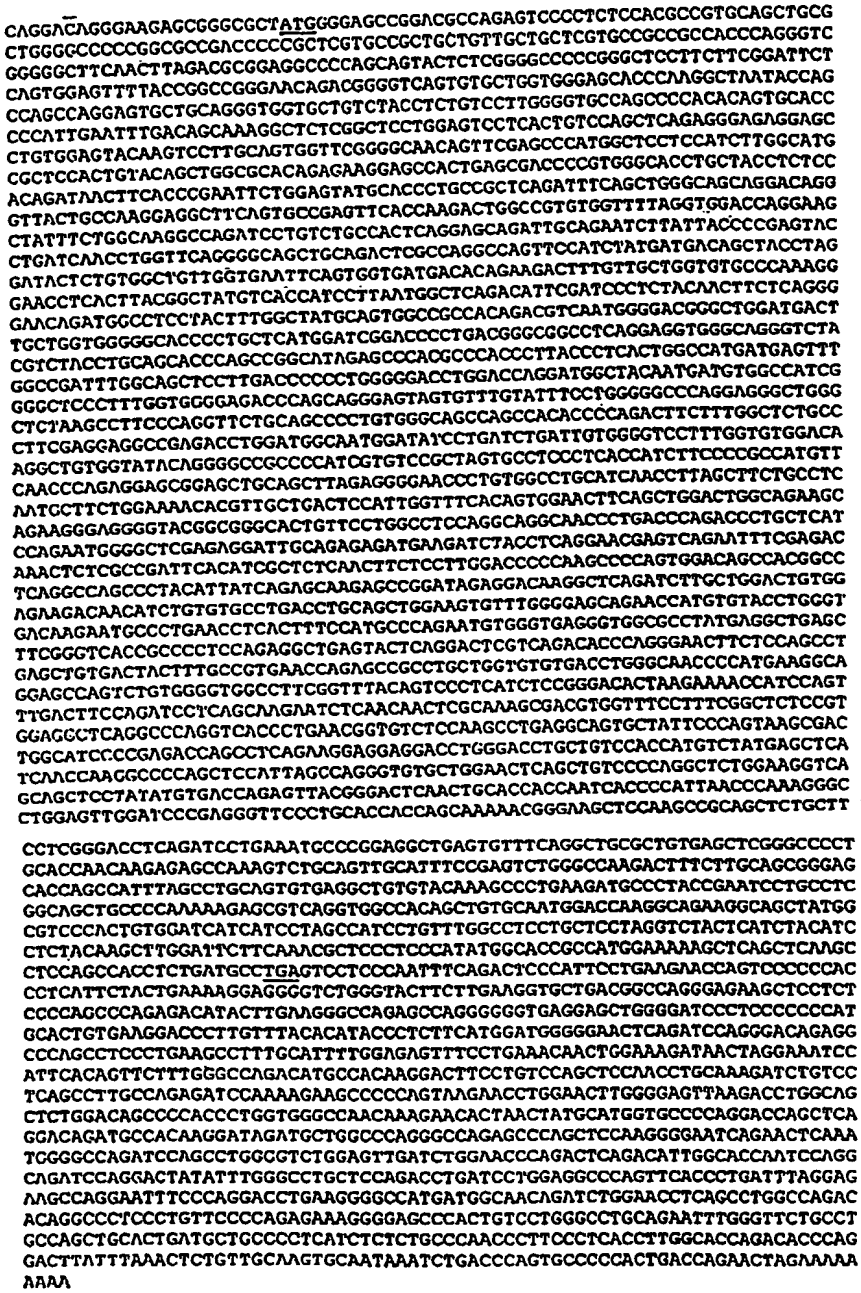

FIGURE 18

MGSRTPESPLHAVQLRWGPRRRPPLVPLLLLLVPPPPRVGGFNLDAEAPAVLSGPPGSFFGFSVEFYRPGTDGVSVLVGA
PKANTSQPGVLQGGAVYLCPWGASPTQCTPIEFDSKGSRLLESSLSSSEGEEPVEYKSLQWFGATVRAIIGSSILACAPLY
SWRTEKEPLSDPVGTCYLSTDNFTRILEYAPCRSDFSWAAGQGYCQGGFSAEFTKTGRVVLGGPGSYFWQGQILSATQEQ
IAESYYPEYLINLVQGQLQTRQASSIYDDSYLGYSVAVGEFSGDDTEDFVAGVPKGNLTYGYVTILNGSDIRSLYNFSGE
QMASYFGYAVAATDVNGDGLDDLLVGAPLLMDRTPDGRPQEVGRVYVYLQHPAGIEPTPTLTLTGHDEFGRFGSSLTPLG
DLDQDGYNDVAIGAPFGGETQQGVVFVFPGGPGGLGSKPSQVLQPLWAASHTPDFFGSALRGGRDLDGNGYPDLIVGSFG
VDKAVVYRGRPIVSASASLTIFPAMFNPEERSCSLEGNPVACINLSFCLNASGKHVADSIGFTVELQLDWQKQKGGVRRA
LFLASRQATLTQTLLIQNGAREDCREMKIYLRNESEFRDKLSPIHIALNFSLDPQAPVDSHGLRPALHYQSKSRIEDKAQ
ILLDCGEDNICVPDLQLEVFGEQNHVYLGDKNALNLTFHAQNVGEGGAYEAELRVTAPPEAEYSGLVRHPGNFSSLSCDY
FAVNQSRILVCDLGNPMKAGASLWGGLRFTVPHLRDTKKTIQFDFQILSKNLNNSQSDVVSFRLSVEAQAQVTLNGVSKP
EAVLFPVSDWHPRDQPQKEEDLGPAVHHVYELINQGPSSISQGVLELSCPQALEGQQLLYVTRVTGLNCTTNHPINPKGL
ELDPEGSLHHQQKRFAPSRSSASSGPQILKCPEAECFRLRCELGPLHQQESQSLQLHFRVWAKTFLQREHQPFSLQCEAV
YKALKMPYRILPRQLPQKERQVATAVQWTKAEGSYGVPLWIIILAILFGLLLLGLLIYILYKLGFFKRSLPYGTAMEKAQ
LKPPATSDA

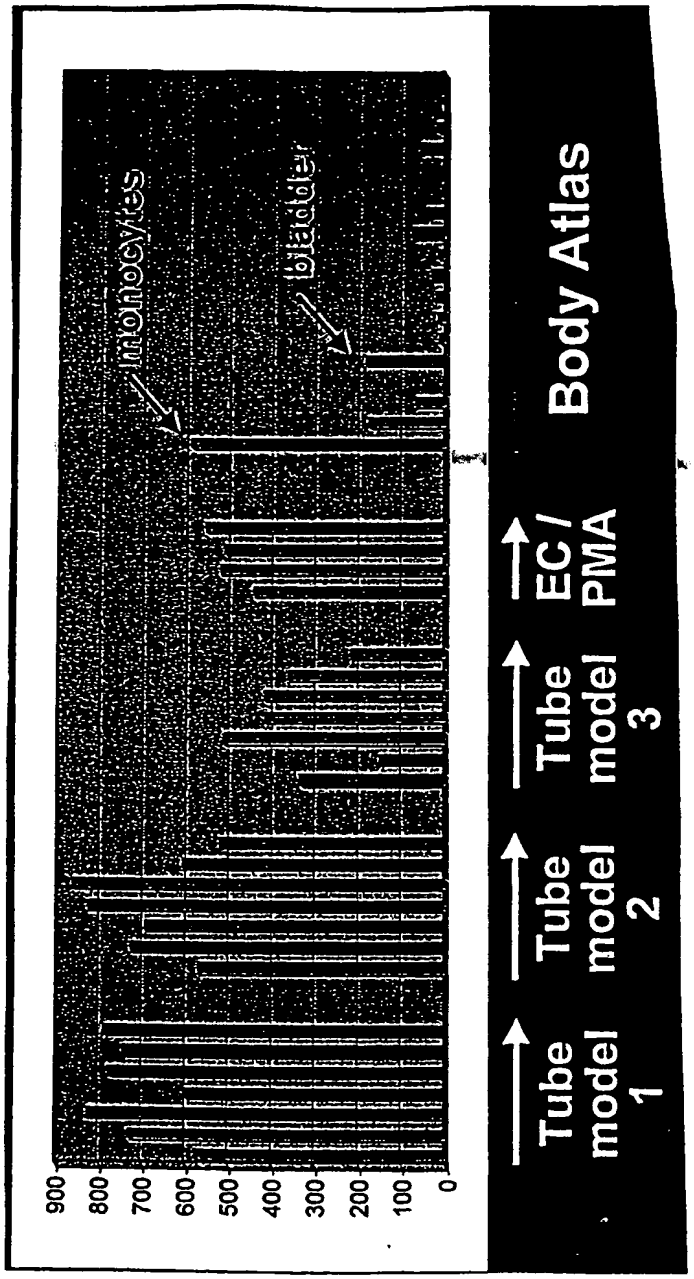


FIGURE 19

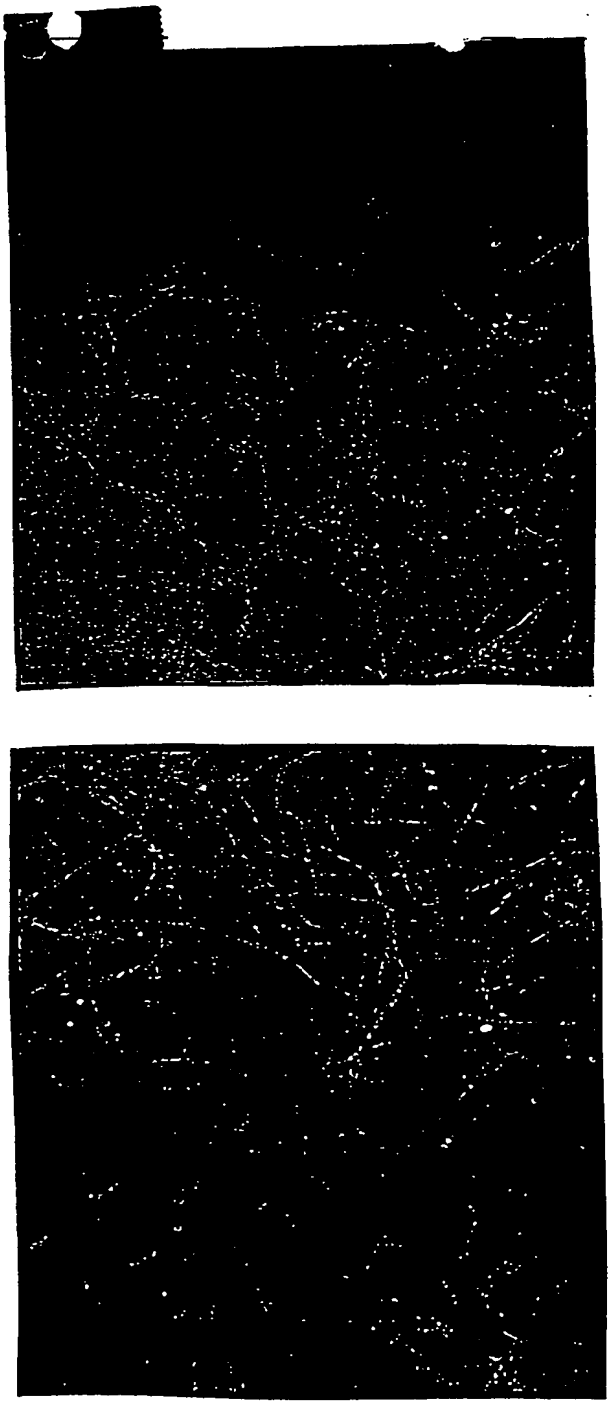

FIGURE 20

## AAA9 cDNA Sequence

AAGGCCCTGCCAGCTTGGGAGGGAATTGTCCCTGCCTGCTTCTGGAGAAAGAAGATATTGACACCATCTAC
GGGCACC[redacted]GAACTGCTTCAAGTGACCATTCTTTTTCTTCTGCCCAGTATTTGCAGCAGTAACAGCACAG
GTGTTTTAGAGGCAGCTAATAATTCACTTGTTGTTACTACAACAAAACCATCTATAACAACACCAAACACA
GAATCATTACAGAAAAATGTTGTCACACCAACAACTGGAACAACTCCTAAAGGAACAATCACCAATGAATT
ACTTAAAATGTCTCTGATGTCAACAGCTACTTTTTTAACAAGTAAAGATGAAGGATTGAAAGCCACAACCA
CTGATGTCAGGAAGAATGACTCCATCATTTCAAACGTAACAGTAACAAGTGTTACACTTCCCAATGCTGTT
TCAACATTACAAAGTTCCAAACCCAAGACTGAAACTCAGAGTTCAATTAAAACAACAGAAATACCAGGTAG
TGTTCTACAACCAGATGCATCACCTTCTAAAACTGGTACATTAACCTCAATACCAGTTACAATTCCAGAAA
ACACCTCACAGTCTCAAGTAATAGRCACTGAGGGTGGAAAAAATGCAAGCACTTCAGCAACCAGCCGGTCT
TATTCCAGTATTATTTTGCCGGTGGTTATTGCTTTGATTGTAATAACACTTTCAGTATTTGTTCTGGTGGG
TTTGTACCGAATGTGCTGGAAGGCAGATCCGGGCACACCAGAAAATGGAAATGATCAACCTCAGTCTGATA
AAGAGAGCGTGAAGCTTCTTACCGTTAAGACAATTTCTCATGAGTCTGGTGAGCACTCTGCACAAGGAAAA
ACCAAGAAC[redacted]CAGCTTGAGGAATTCTCTCCACACCTAGGCAATAATTACGCTTAATCTTCAGCTTCTAT
GCACCAAGCGTGGAAAAGGAGAAAGTGGTGGAGAATGAATGCCGAGTTCGATAGGTGGTGCTGGAGTGTAG
CAGACGTCTGTCCCAGTAAAGTGATGTCCAGCTGACATGCAATAATTTGATGGAATCAAAAAGAACCCCGG
GGCTCTCCTGTTCTCTCACATTTAAAAATTCCATTACTCCATTTACAGGAGCGTTCCTAGGAAAAGGAATT
TTAGGAGGAGAATTTGTGAGCAGTGAATCTGACAGCCCAGGAGGTGGGCTCGCTGATAGGCATGACTTTCC
TTAATGTTTAAAGTTTTCCGGGCCAAGAATTTTTATCCATGAAGACTTTCCTACTTTTCTCGGTGTTCTTA
TATTACCTACTGTTAGTATTTATTGTTTACCACTATGTTAATGCAGGGAAAAGTTGCACGTGTATTATTAA
ATATTAGGTAGAAATCATACCATGCTACTTTGTACATATAAGTATTTTATTCCTGCTTTCGTGTTACTTTT
AATAAATAACTACTGTACTCAATACTCTAAAAATACTATAACATGACTGTGAAAATGGCAATGTTATTGTC
TTCCTATAATTATGAATATTTTTGGATGGATTATTAGAATACATGAACTCACTAATGAAAGGCATTTGTAA
TAAGTCAGAAAGGGACATAGGATTCACATATCAGACTGTTAGGGGGAGAGNTAATTATCAGTTCTTTGGTC
TTTCTATTTGTCATTCATACTATGTGATGAAGATGTAAGTGCAAGGGCATTTATAACACTATACTGCATTC
ATTAGATAT

FIGURE 21

## AAA9 Protein

MEILQVTILPLEPSTCSSNSTGVLEAANNSLVVTTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLK
MSLMSTATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQSSKPKTETQSSIKTTEIPGSVL
QPDASPSKTGTLTSIPVTIPENTSQSQVIXTEGGKNASTSATSRSYSSIILP[redacted]Y
RMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEHSAQGKTKN

FIGURE 22

# AAB4 (MMP10)

ATGCATCTTGCATTCCTTGTGCTGTTGTGTCTGCCAGTCTGCTCTGCCTATCCTCTGAGTGGGG
CAGCAAAAGAGGAGGACTCCAACAAGGATCTTGCCCAGCAATACCTAGAAAAGTACTACAAC
CTCGAAAAGGATGTGAAACAGTTTAGAAGAAAGGACAGTAATCTCATTGTTAAAAAAATCCA
AGGAATGCAGAAGTTCCTTGGGTTGGAGGTGACAGGGAAGCTAGACACTGACACTCTGGAGG
TGATGCGCAAGCCCAGGTGTGGAGTTCCTGACGTTGGTCACTTCAGCTCCTTTCCTGGCATGCC
GAAGTGGAGGAAAACCCACCTTACATACAGGATTGTGAATTATACACCAGATTTGCCAAGAG
ATGCTGTTGATTCTGCCATTGAGAAAGCTCTGAAAGTCTGGGAAGAGGTGACTCCACTCACAT
TCTCCAGGCTGTATGAAGGAGAGGCTGATATAATGATCTCTTTCGCAGTTAAAGAACATGGAG
ACTTTTACTCTTTTGATGGCCCAGGACACAGTTTGGCTCATGCCTACCCACCTGGACCTGGGCT
TTATGGAGATATTCACTTTGATGATGATGAAAAATGGACAGAAGATGCATCAGGCACCAATTT
ATTCCTCGTTGCTGCTCATGAACTTGGCCACTCCCTGGGGCTCTTTCACTCAGCCAACACTGAA
GCTTTGATGTACCCACTCTACAACTCATTCACAGAGCTCGCCCAGTTCCGCCTTTCGCAAGATG
ATGTGAATGGCATTCAGTCTCTCTACGGACCTCCCCCTGCCTCTACTGAGGAACCCCTGGTGCC
CACAAAATCTGTTCCTTCGGGATCTGAGATGCCAGCCAAGTGTGATCCTGCTTTGTCCTTCGAT
GCCATCAGCACTCTGAGGGGAGAATATCTGTTCTTTAAAGACAGATATTTTTGGCGAAGATCC
CACTGGAACCCTGAACCTGAATTTCATTTGATTTCTGCATTTTGGCCCTCTCTTCCATCATATTT
GGATGCTGCATATGAAGTTAACAGCAGGGACACCGTTTTTATTTTTAAAGGAAATGAGTTCTG
GGCCATCAGAGGAAATGAGGTACAAGCAGGTTATCCAAGAGGCATCCATACCCTGGGTTTTC
CTCCAACCATAAGGAAAATTGATGCAGCTGTTTCTGACAAGGAAAAGAAGAAAACATACTTC
TTTGCAGCGGACAAATACTGGAGATTTGATGAAAATAGCCAGTCCATGGAGCAAGGCTTCCCT
AGACTAATAGCTGATGACTTTCCAGGAGTTGAGCCTAAGGTTGATGCTGTATTACAGGCATTT
GGATTTTTCTACTTCTTCAGTGGATCATCACAGTTTGAGTTTGACCCCAATGCCAGGATGGTGA
CACACATATTAAAGAGTAACAGCTGGTTACATTGCTCTAGAAAA

FIGURE 23

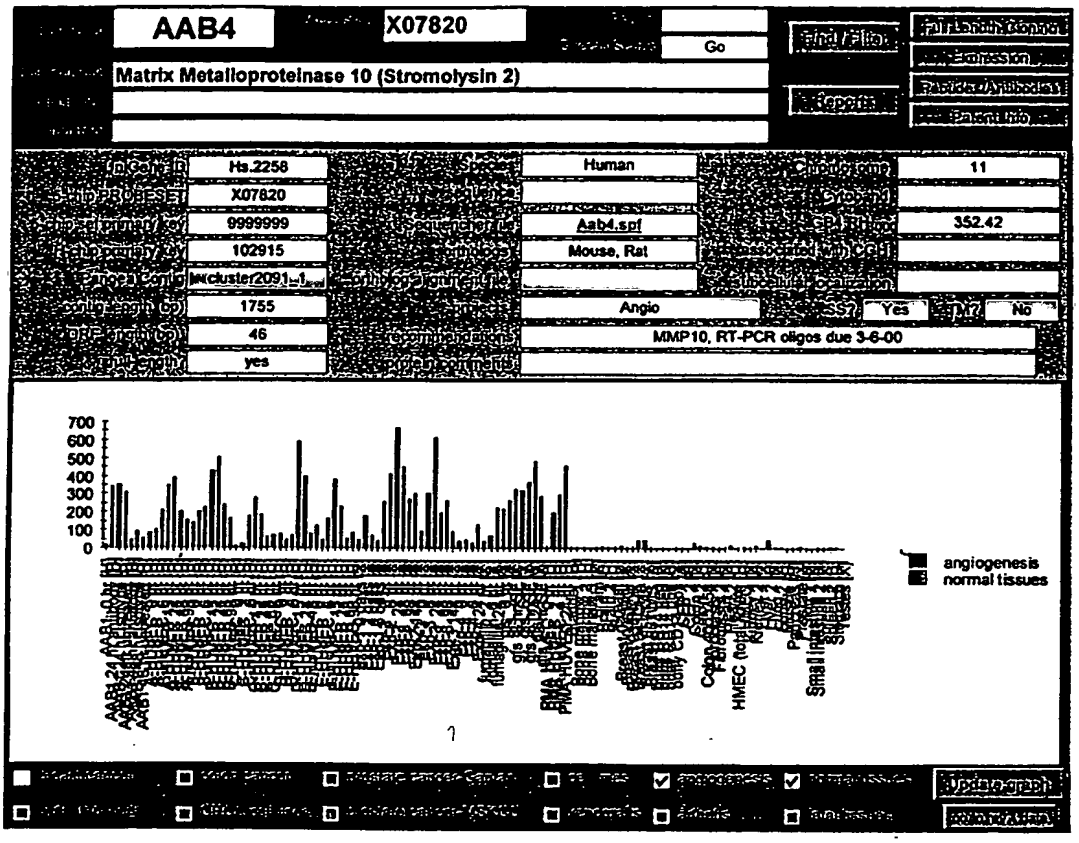


FIGURE 24

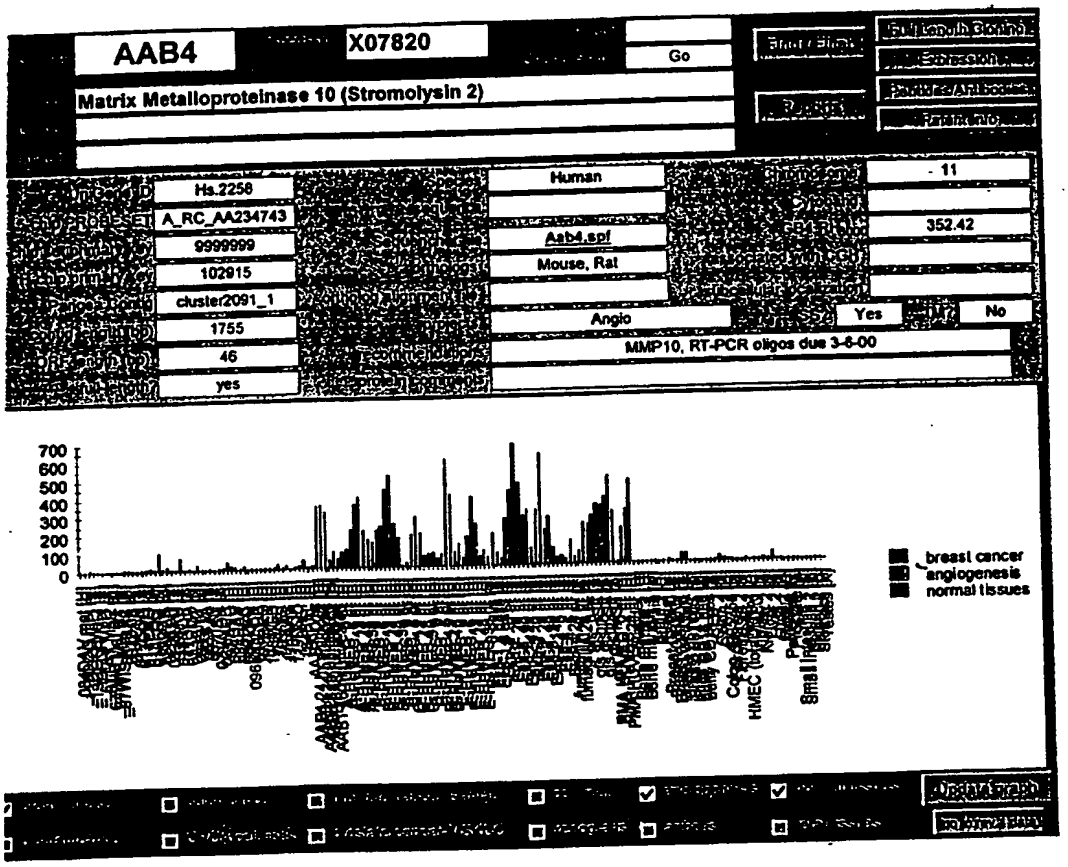
AAB4
X07820
Go
Matrix Metalloproteinase 10 (Stromolysin 2)
Hs.2258
A_RC_AA234743
9999999
102915
cluster2091_1
1755
46
yes
Human
Aab4.spf
Mouse, Rat
Angio
11
352.42
Yes
No
MMP10, RT-PCR oligos due 3-6-00
700
600
500
400
300
200
100
0
breast cancer
angiogenesis
normal tissues

FIGURE 25